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# OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:15 ; Search time 221.345 Seconds  
(without alignments)  
311.909 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830

Sequence: 1 MFQDPQRPRKLPQLCTELQ.....WTGRKMSCCRSRRRTETQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

A: Geneseq 8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	828	99.8	248	8	AD044062 Amino aci
2	828	99.8	248	8	AD044064 Amino aci
3	826	99.5	151	6	AAO22640 HPV-16 pr
4	826	99.5	151	6	AAO22636 HPV prote
5	826	99.5	151	8	AD044072 Amino aci
6	826	99.5	162	2	AAW35742 Human pap
7	826	99.5	248	8	AD044060 Amino aci
8	823	99.2	151	8	ADU66364 Human pap
9	823	99.2	158	2	AAK22766 HPV E6 pe
10	823	99.2	158	3	AAV82462 Human pap
11	823	99.2	158	4	AAV82420 Human pap
12	823	99.2	158	7	ADP09515 Human pap
13	823	99.2	158	8	ADU66363 Human pap
14	823	99.2	158	9	AE40817 Anti-apop
15	823	99.2	158	9	AE40817 Anti-apop
16	823	99.2	158	9	AE40817 Anti-apop
17	823	99.2	158	9	AE40817 Anti-apop
18	823	99.2	158	9	AE40817 Anti-apop
19	823	99.2	158	9	AE40817 Anti-apop
20	823	99.2	158	9	AE40817 Anti-apop
21	823	99.2	158	9	AE40817 Anti-apop
22	823	99.2	158	9	AE40817 Anti-apop
23	823	99.2	158	9	AE40817 Anti-apop

24	823	99.2	248	8	AD044070 Amino aci
25	823	99.2	256	8	ADR47005 Human pap
26	823	99.2	256	10	AE40157 Human pap
27	823	99.2	266	2	AAK22725 HPV 16 E6
28	823	99.2	266	2	AAK22725 HPV 16 E6
29	823	99.2	273	2	AAV25376 HPV fusio
30	823	99.2	273	2	AAV25376 HPV fusio
31	823	99.2	273	2	AAV25376 HPV fusio
32	823	99.2	292	2	AAV25379 HPV fusio
33	823	99.2	292	2	AAV25379 HPV fusio
34	823	99.2	292	2	AAV25379 HPV fusio
35	823	99.2	371	2	AAV25377 HPV fusio
36	823	99.2	371	2	AAV25377 HPV fusio
37	823	99.2	371	2	AAV25377 HPV fusio
38	823	99.2	390	2	AAV25381 HPV fusio
39	823	99.2	390	2	AAV25381 HPV fusio
40	823	99.2	390	2	AAV25381 HPV fusio
41	821	98.9	248	8	AD044066 Amino aci
42	818	98.6	151	3	AAV57808 HPV-16 E6
43	815	98.2	158	8	ADL90078 Human pap
44	779.5	93.9	243	2	AAW99369 Papilloma
45	580	69.9	149	2	AAK40919 HPV E6 re

## ALIGNMENTS

RESULT 1	AD044062	AD044062 standard; protein; 248 AA.
ID	AD044062	
XX	AD044062	
AC	AD044062	
DT	15-JUL-2004	(first entry)
DE	Amino acid sequence of a fusion protein designated E6E7Retm.	
KM	E6 protein; E7 protein; fusion protein; HPV16, HPV-associated cancer;	
KW	cervical cancer; immune response; lower gastrointestinal tract cancer;	
XX	anal cancer; reproductive system cancer; penile cancer; vulvar cancer.	
OS	Human papillomavirus type 16.	
XX	Synthetic.	
FN	WO2004030636-A2.	
PD	15-APR-2004.	
PF	02-OCT-2003; 2003US-0415929P.	
XX	03-OCT-2002; 2002US-0415929P.	
XX	(AMHP) WYETH HOLDINGS CORP.	
XX	Smith L, Cassetti MC;	
XX	WPI; 2004-316328/29.	
XX	N-PSDB; AD044063.	
PT	New polypeptide comprising human papillomavirus E6 and E7 polypeptides,	
PT	useful for treating or preventing human papillomavirus (HPV)-associated	
PT	cancers, e.g. cervical cancer.	
XX	Claim 22; Page 68-69; 10pp; English.	
XX	The present sequence represents a fusion protein, comprising E6 and E7	
XX	polypeptides from human papillomavirus type 16 (HPV16). The fusion	
XX	protein is designated E6E7Retm, and comprises an E6 amino terminus (where	
XX	residues 63 and 106 have been replaced with glycine) and an E7 carboxy	
XX	terminus (where residues 24 and 26 have been replaced with glycine).	
XX	E6E7Retm is representative of fusion proteins of the invention. The	
XX	specification describes human papillomavirus E6 and E7 polypeptides,	
XX	where the E7 polypeptide has mutations at any one or more of the amino	

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC the sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.8%; Score 828; DB 8; Length 248;

Best Local Similarity 98.7%; Pred. No. 4.6e-84; Mismatches 149; Conservative 0; Indels 2; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRLDCTVYRDGNPY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRLDCTVYRDGNPY 60  
QY 61 AVXDCKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRCIHXQKPLCPBEKQRHLD 120  
DB 61 AVGDCKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRCIHXQKPLCPBEKQRHLD 120  
QY 121 KKQRFNIRGRWTCSCCRSSRTRETQL 151  
DB 121 KKQRFNIRGRWTCSCCRSSRTRETQL 151

RESULT 2

ADO44064 ADO44064 standard; protein; 248 AA.

XX ADO44064;

DT 15-JUL-2004 (first entry)

XX Amino acid sequence of a fusion protein designated E6E7PentM.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
XX cervical cancer; immune response; lower gastrointestinal tract cancer;  
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX Human papillomavirus type 16.  
XX Synthetic.

OS WO2004030636-A2.

PN 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP ) WYETH HOLDINGS CORP.

XX Smith L, Caesetti MC;

XX WPI; 2004-316328/29.

DR N-PSDB; ADO44065.

XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
XX useful for treating or preventing human papillomavirus (HPV)-associated  
XX cancers, e.g. cervical cancer.

PS Claim 22; Page 70-71; 101pp; English.

XX The present sequence represents a fusion protein, comprising E6 and E7  
XX polypeptides from human papillomavirus type 16 (HPV16). The fusion  
XX protein is designated E6E7PentM, and comprises an E6 amino terminus  
XX (where residues 63 and 106 have been replaced with glycine) and an E7  
XX carboxy terminus (where residues 24, 26 and 91 have been replaced with

CC glycine). E6E7PentM is representative of fusion proteins of the  
CC invention. The specification describes human papillomavirus E6 and E7  
CC polypeptides, where the E7 polypeptide has mutations at any one or more  
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the  
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has  
CC mutations at any one or more of the amino acids corresponding to amino  
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of  
CC the invention are useful for treating or preventing human papillomavirus  
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins  
CC and nucleic acids encoding the fusion proteins are useful for generating  
CC immune responses against HPV. They are also useful for treating lower  
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of  
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.8%; Score 828; DB 8; Length 248;

Best Local Similarity 98.7%; Pred. No. 4.6e-84; Mismatches 149; Conservative 0; Indels 2; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRLDCTVYRDGNPY 60  
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRLDCTVYRDGNPY 60  
QY 61 AVXDCKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRCIHXQKPLCPBEKQRHLD 120  
DB 61 AVGDCKLKFYSKISEYRHVCYSYVGTTLLEQYNNKPLCDLLIRCIHXQKPLCPBEKQRHLD 120  
QY 121 KKQRFNIRGRWTCSCCRSSRTRETQL 151  
DB 121 KKQRFNIRGRWTCSCCRSSRTRETQL 151

RESULT 3

AAO22640 AAO22640 standard; protein; 151 AA.

XX AAO22640;

DT 15-MAY-2003 (first entry)

XX HPV-16 protein sequence, SEQ ID NO 27.

XX Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;  
XX cancer; human papilloma virus; cervix; cell-mediated immune response;  
XX HPV; HPV-16.

XX Human papilloma virus.

XX WO2003008649-A1.

PN 30-JAN-2003.

XX 19-JUL-2002; 2002WO-US023198.

XX 20-JUL-2001; 2001US-0306809P.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Sastry KJ, Tortolero-Luna G, Follen M;

XX WPI; 2003-239363/23.

XX Determining a possible recurrence of a (pre-)cancerous growth in a  
XX patient infected with human papilloma virus (HPV), comprises incubating  
XX the sample with an HPV E6 or E7 peptide and detecting a cell-mediated  
XX immune response.

PS Disclosure; Page 129-130; 132pp; English.

XX The invention relates to a novel method for determining the possibility  
XX of recurrence of a (pre-)cancerous growth in a patient infected with  
XX human papilloma virus (HPV) or suspected of being infected with HPV, and

CC has or had a (pre-)cancerous growth on or around the cervix. The novel  
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from  
CC the patient, and assaying the sample for a cell-mediated immune response  
CC against the peptide. The method is useful for determining the possibility  
CC and preventing the recurrence of a (pre-)cancerous growth in a patient  
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or  
CC E7 peptides are useful in immunotherapy for the preventing or reducing  
CC the risk of development of (pre-)cancerous growths. This sequence  
CC represents an HPV-16 protein of the invention

SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;

Best Local Similarity 98.7%; Pred. No. 4.2e-84; Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDPAFADLCIVRDGMPY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDPAFADLCIVRDGMPY 60  
QY 61 AVXDCKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCEEKQRHLD 120  
DB 61 AVXDCKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCEEKQRHLD 120  
QY 121 KKORFHNIRGRWGTGRCMSCRSSRTRRETOL 151  
DB 121 KKORFHNIRGRWGTGRCMSCRSSRTRRETOL 151

RESULT 4

AAO22636 ID AAO22636 standard; protein; 151 AA.

AC AAO22636;

DT 15-MAY-2003 (first entry)

DE HPV protein sequence, SEQ ID No 20.

XX Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;  
KW cancer; human papilloma virus; cervix; cell-mediated immune response;  
KW HPV; HPV-16.

OS Human papilloma virus.

WO2003008649-A1.

30-JAN-2003.

19-JUL-2002; 2002WO-US023198.

20-JUL-2001; 2001US-0306809P.

(TEXA ) UNIV TEXAS SYSTEM.

Sastiy KI, Tortolero-Luna G, Follen M;

WPI; 2003-239363/23.

PT Determining a possible recurrence of a (pre-)cancerous growth in a  
PT patient infected with human papilloma virus (HPV), comprises incubating  
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated  
PT immune response.

XX Disclosure; Page 125-126; 132pp; English.

CC The invention relates to a novel method for determining the possibility  
CC of recurrence of a (pre-)cancerous growth in a patient infected with  
CC human papilloma virus (HPV) or suspected of being infected with HPV, and  
CC has or had a (pre-)cancerous growth on or around the cervix. The novel  
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from  
CC the patient, and assaying the sample for a cell-mediated immune response  
CC against the peptide. The method is useful for determining the possibility

CC and preventing the recurrence of a (pre-)cancerous growth in a patient  
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or  
CC E7 peptides are useful in immunotherapy for the preventing or reducing  
CC the risk of development of (pre-)cancerous growths. This sequence  
CC represents an HPV protein of the invention

SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;

Best Local Similarity 98.7%; Pred. No. 4.2e-84; Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDPAFADLCIVRDGMPY 60  
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDPAFADLCIVRDGMPY 60  
QY 61 AVXDCKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCEEKQRHLD 120  
DB 61 AVXDCKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLIRCIINXQKPLCEEKQRHLD 120  
QY 121 KKORFHNIRGRWGTGRCMSCRSSRTRRETOL 151  
DB 121 KKORFHNIRGRWGTGRCMSCRSSRTRRETOL 151

RESULT 5

ADO44072 ID ADO44072 standard; protein; 151 AA.

AC ADO44072;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a wild type HPV16 E6 protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 16.

WO2004030636-A2.

15-APR-2004.

02-OCT-2003; 2003WO-US031726.

03-OCT-2002; 2002US-0415929P.

(AMHP ) WYETH HOLDINGS CORP.

Smith L, Caesetti MC;

WPI; 2004-316326/29.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
PT useful for treating or preventing human papillomavirus (HPV)-associated  
PT cancers, e.g. cervical cancer.

PS Claim 1; Page 76-77; 101pp; English.

CC The present sequence represents a wild type E6 protein from human  
CC papillomavirus type 16 (HPV16), which is used to produce fusion proteins  
CC of the invention. The specification describes human papillomavirus E6 and  
CC E7 polypeptides, where the E7 polypeptide has mutations at any one or  
CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the  
CC sequence given in ADO44072 and the E6 polypeptide has no mutations or has  
CC mutations at any one or more of the amino acids corresponding to amino  
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of  
CC the invention are useful for treating or preventing human papillomavirus  
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins  
CC and nucleic acids encoding the fusion proteins are useful for generating

CC immune responses against HPV. They are also useful for treating lower  
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of  
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 151 AA;

Query Match 99.5%; Score 826; DB 8; Length 151;

Best Local Similarity 98.7%; Pred. No. 4,2e-84;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFDLCIVRDGNPY 60

Db 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFDLCIVRDGNPY 60

Qy 61 AVXDKCLKFYSKISEYHRYCYSVYGTTLLEQYNNKPLCDLLIRCIHXKQPLCPBEKQRHLD 120

Db 61 AVXDKCLKFYSKISEYHRYCYSVYGTTLLEQYNNKPLCDLLIRCIHXKQPLCPBEKQRHLD 120

Qy 121 KQRFNHNIRGRWTRGCMSCCRSSRTRETOL 151

Db 121 KQRFNHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 6

AAW35742 ID AAW35742 standard; protein; 162 AA.

XX AAW35742;

DT 25-MAR-2003 (revised)

DT 16-FEB-1998 (first entry)

DE Human papillomavirus type 16 E6 protein variant.

KW Complete genome; circular; human papillomavirus type 16; HPV16 E6;

XX cervical dysplasia; cervical cancer; cervical smear.

OS Human papillomavirus type 16.

XX Key Location/Qualifiers

FT Misc-difference 90 /note= "Mutated from leu in the reference sequence

FT Misc-difference 159 /note= "End of protein sequence even though 3 amino acid

FT residues are given following on"

XX US5679509-A.

XX 21-OCT-1997.

XX 30-SEP-1994; 94US-00316239.

XX 28-SEP-1993; 93US-00127906.

XX (UTNE-) UNIV NEW MEXICO STATE.

XX Wheeler CM, Parmenter CA;

XX WPI; 1997-525714/48.

XX N-PSDB; AAT94742.

PT Evaluating risk of cervical dysplasia or cervical cancer - by detecting

XX variant form of human papilloma virus 16.

XX Claim 7; Col 23-26; 33pp; English.

XX Methods have been developed for distinguishing a subset of human

CC papilloma virus (HPV) that is associated with an increased risk of

CC developing cervical dysplasia or cervical cancer. The methods involve:

CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the

CC sample and determining if the base at position 350 of the E6 gene (see

CC at position 350 is associated with an increased risk of developing

CC cervical dysplasia or cervical cancer; and (2) preparing a cervical

CC sample to expose any HPV-16 E6 protein in the sample and determining if

CC the amino acid at position 83 of the protein (see position 90 in AAW35741

CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at

CC position 83 that is associated with an increased risk of developing

CC cervical dysplasia or cervical cancer. The present sequence represents

CC the variant protein sequence for HPV-16 E6. The 350G variant correlates

CC well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4

CC for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;

CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 162 AA;

Query Match 99.5%; Score 826; DB 2; Length 162;

Best Local Similarity 98.7%; Pred. No. 4.6e-84;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFDLCIVRDGNPY 60

Db 8 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFDLCIVRDGNPY 67

Qy 61 AVXDKCLKFYSKISEYHRYCYSVYGTTLLEQYNNKPLCDLLIRCIHXKQPLCPBEKQRHLD 120

Db 68 AVXDKCLKFYSKISEYHRYCYSVYGTTLLEQYNNKPLCDLLIRCIHXKQPLCPBEKQRHLD 127

Qy 121 KQRFNHNIRGRWTRGCMSCCRSSRTRETOL 151

Db 128 KQRFNHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 7

ADO44060 ID ADO44060 standard; protein; 248 AA.

XX ADO44060;

XX 15-JUL-2004 (first entry)

DE Amino acid sequence of an E6E7 fusion protein.

KW E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;

XX cervical cancer; immune response; lower gastrointestinal tract cancer;

XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 16.

XX Synthetic.

XX WO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP ) WYETH HOLDINGS CORP.

XX Smith L, Cassetti MC;

XX WPI; 2004-316328/29.

XX N-PSDB; ADO44061.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,

XX useful for treating or preventing human papillomavirus (HPV)-associated

XX cancers, e.g. cervical cancer.

XX Example 1; Page 67-68; 101pp; English.

XX The present sequence represents an E6E7 fusion protein, comprising wild

XX type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16).

XX The specification describes human papillomavirus E6 and E7 polypeptides,

XX where the E7 polypeptide has mutations at any one or more of the amino

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC the sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancer, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.5%; Score 826; DB 8; Length 248;

Best Local Similarity 98.7%; Pred. No. 7.7e-84; Mismatches 149; Conservative 0; Indels 0; Gaps 0;

QY 1 MFQDPQEPKRLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGMPY 60  
DB 1 MFQDPQEPKRLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGMPY 60

QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCTNXQKPLCPBEKQRHLD 120  
DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCTNXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 8

ID ADO66364 standard; protein; 151 AA.

XX ADU66364;

DT 10-FEB-2005 (first entry)

XX Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 5.

XX vaccine; MHC class I pathway; antigen specific immune response; tumor;  
KM E7 protein; E6 protein.

OS Human papillomavirus type 16.

XX WO2004098526-A2.

PN 18-NOV-2004.

PF 05-MAY-2004; 2004WO-US013756.

XX 05-MAY-2003; 2003US-0467602P.

XX (UYJO ) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF;

XX WPI; 2004-813972/80.

PT New nucleic acid molecules encoding a fusion polypeptide comprising an  
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine  
PT for inducing or enhancing immune response or for inhibiting or preventing  
PT tumor growth.

XX Disclosure; SEQ ID NO 5; 67bp; English.

XX The invention comprises a nucleic acid molecule (DNA vaccine) that  
CC encodes a fusion polypeptide which is useful as a vaccine composition.  
CC The nucleic acid of the invention contains: a first nucleic acid encoding  
CC a polypeptide that promotes processing via the MHC class I pathway; a  
CC second sequence encoding a signal peptide; and a third sequence encoding  
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for  
CC inducing or enhancing an antigen specific immune response, or to inhibit

CC growth or prevent re-growth of a tumor expressing Human papillomavirus  
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a  
CC human papillomavirus type 16 (HPV16) E6 protein of the invention.

XX Sequence 151 AA;

Query Match 99.2%; Score 823; DB 8; Length 151;

Best Local Similarity 98.0%; Pred. No. 9.2e-84; Mismatches 148; Conservative 1; Indels 2; Gaps 0;

QY 1 MFQDPQEPKRLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGMPY 60  
DB 1 MFQDPQEPKRLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGMPY 60

QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCTNXQKPLCPBEKQRHLD 120  
DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCTNXQKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 9

ID AAR22766 standard; peptide; 158 AA.

XX AAR22766;

DT 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX HPV E6 peptide.

XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.

XX Synthetic.

OS Homo sapiens.

PN WO9205248-A.

XX 02-APR-1992.

XX 26-SEP-1991; 91WO-US007081.

XX 26-SEP-1990; 90US-00588384.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;

XX WPI; 1992-132119/16.

PT Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and  
PT recombinant cells encoding them, useful in treatment and prophylaxis of  
PT cervical warts or cancer resulting from HPV infection.

XX Disclosure; Fig 7; 81bp; English.

XX The peptide is the sequence of the human papillomavirus HPV 16 E6  
CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)  
CC of HPV 16 E6 were synthesized by standard Merrifield synthesis. Examples  
CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions  
CC contg. these peptides, antibodies against the peptides, or recombinant  
CC cells contg. the gene encoding the immuno- genic peptides may be utilised  
CC in methods for inhibiting and treating HPV infection and tumour  
CC initiation and progression e.g. in the prevention or retardation of  
CC cervical warts and cervical carcinoma resulting from HPV infection. See  
CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on  
CC 25-MAR-2003 to correct PI field.)

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 2; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYVCKQQLLRREYDFAFRDLCTIVRDGMPY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIILECYVCKQQLLRREYDFAFRDLCTIVRDGMPY 67

QY 61 AVXDCKLKFYSKISEYHNYCYSVGTTLBEOQYNKPLCDLLIRCIHXKQKPLCPBEKQRLD 120  
DB 68 AVCDCKLKFYSKISEYHNYCYSLVGTTLBEOQYNKPLCDLLIRCIHXKQKPLCPBEKQRLD 127

QY 121 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 151  
DB 128 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 158

RESULT 10  
AAY82462  
ID AAY82462 standard; protein; 158 AA.  
XX  
AC AAY82462;  
XX  
DT 30-JUN-2000 (first entry)  
XX  
DE Human papillomavirus E6 protein containing two zinc finger motifs.  
XX  
KM Chelated zinc finger; therapeutic; treatment; prophylaxis; HPV;  
KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;  
KW wart.  
XX  
OS Human papillomavirus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 37..73  
FT /note= "forms a zinc finger motif"  
FT Misc-difference 110..146  
FT /note= "forms a zinc finger motif"  
XX  
PN WO200014063-A1.  
XX  
PD 16-MAR-2000.  
XX  
PF 03-SEP-1999; 99WO-AU000724.  
XX  
PR 04-SEP-1998; 98AU-00005733.  
PR 15-JUL-1999; 99AU-00001645.  
XX  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
PA (HUGH/) HUGHES E J L.  
XX  
PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;  
XX  
DR WPI; 2000-256917/22.  
XX  
PT Polyulfide and dithionodisulfide agents, useful for the treatment or  
PT prophylaxis of diseases caused by mammalian papillomavirus, are  
PT disruptors of a chelated metal cation domain in an HPV gene encoded  
PT protein.  
XX  
PS Disclosure; Fig 1; 78pp; English.  
XX  
CC The present invention describes an agent used in the treatment or  
CC prophylaxis of a disease caused or exacerbated by HPV (mammalian  
CC papillomavirus) comprising a compound capable of reducing, inhibiting or  
CC otherwise decreasing the activity of a protein encoded by an HPV gene by  
CC facilitating disruption of a chelated metal cation domain present in the  
CC protein. An agent of the present invention can be used to treat cervical  
CC cancer or its HPV associated precursor lesions or other HPV associated  
CC cancers and/or warts. The present sequence represents a human  
CC papillomavirus E6 protein containing two zinc finger motifs, as given in  
CC the exemplification of the present invention  
XX

SQ Sequence 158 AA:  
Query Match 99.2%; Score 823; DB 3; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYVCKQQLLRREYDFAFRDLCTIVRDGMPY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIILECYVCKQQLLRREYDFAFRDLCTIVRDGMPY 67

QY 61 AVXDCKLKFYSKISEYHNYCYSVGTTLBEOQYNKPLCDLLIRCIHXKQKPLCPBEKQRLD 120  
DB 68 AVCDCKLKFYSKISEYHNYCYSLVGTTLBEOQYNKPLCDLLIRCIHXKQKPLCPBEKQRLD 127

QY 121 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 151  
DB 128 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 158

RESULT 11  
AAB98420  
ID AAB98420 standard; protein; 158 AA.  
XX  
AC AAB98420;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
DE Human papillomavirus protein HPV16 E6.  
XX  
KM Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
KW epitope; T cell; identification; vaccine; infection; genital wart;  
KW neoplastic growth; antiviral.  
XX  
OS Human papillomavirus.  
XX  
PN WO200141799-A1.  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000WO-US033549.  
XX  
PR 10-DEC-1999; 99US-0172705P.  
PR 15-AUG-2000; 2000US-00641528.  
XX  
PA (EPIM-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;  
XX  
DR WPI; 2001-381497/40.  
XX  
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
PT treating HPV infections.  
XX  
PS Disclosure; Page 20-21; 756pp; English.  
XX  
CC The present invention describes an isolated prepared human papillomavirus  
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
CC production. Peptides and corresponding nucleic acid compositions from the  
CC present invention are useful for stimulating an immune response to HPV by  
CC stimulating the production of CTL or HTL responses, specifically in the  
CC treatment or prophylaxis of HPV infection, in persons who have not  
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
CC can also be used in a tetramer staining assay to assess peripheral blood  
CC mononuclear cells for the presence of antigen-specific CTLs following  
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
CC compositions are useful for removing warts or treating HPV infections.  
CC The epitopes for inclusion in an epitope-base vaccine may be selected  
CC from conserved regions of viral or tumour-associated antigens, which  
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes  
CC that may be present in whole antigens can be avoided with the use of  
CC epitope-base vaccines. An additional advantage is the ability to combine  
CC selected epitopes (CTL and HTL) and to modify the composition of the

CC epitopes achieving enhanced immunogenicity, the major benefit of the  
CC vaccine is that is safe and efficacious; AAB98391 to AAB98477 represent  
CC polypeptide sequences used in the exemplification of the present  
CC invention

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 4; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSLVGTLEQYKNPCLDILRCINXQKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSLVGTLEQYKNPCLDILRCINXQKPLCPBEKQRHLD 127  
QY 121 KKQRFHNIRGRWTRGCMSCCRSRTRETOL 151  
DB 128 KKQRFHNIRGRWTRGCMSCCRSRTRETOL 158

#### RESULT 12

ID ADF09515 standard; protein; 158 AA.

XX ADF09515;

DT 12-FEB-2004 (first entry)

DE Human papillomavirus 16 E6 SEQ ID NO:16.

KW human; protein-protein interaction; virucide; cytostatic; vaccine;

KM human papilloma virus; HPV; cancer.

OS Human papillomavirus.

PN WO2003068940-A2.

PD 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004594.

PR 14-FEB-2002; 2002US-0356911P.

PA (CURA-) CURAGEN CORP.

PA (HOFF) HOFFMANN LA ROCHE INC.

PI Jackson A, Ooi CE, Lewin DA, Cuthill S;

DR WPI; 2003-689668/65.

DR N-PSDB; ADF09607.

PT New purified complex comprising a first polypeptide and a second  
PT polypeptide, useful for identifying agents for treating/preventing a  
PT condition involving altered level of the complex e.g. human papilloma  
PT virus infection, or cancer.

PS Example 3; SEQ ID NO 16; 156pp; English.

XX The invention relates to a novel purified complex comprising a first  
CC polypeptide and a second polypeptide, where the polypeptides comprise  
CC defined amino acid sequences listed in the specification, and where the  
CC first polypeptide binds to the second polypeptide. A complex of the  
CC invention has virucide and cytostatic activity, and may have a use as a  
CC vaccine. The complex is useful for identifying agents for treating or  
CC preventing a conditions involving altered level of the complex, e.g.  
CC human papilloma virus (HPV) infection, or cancer. The compositions,  
CC antibodies, vectors and methods are useful for treating such diseases.  
CC The sequences shown in ADF09500-ADF09583 represent proteins of the  
CC invention.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 7; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60  
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSLVGTLEQYKNPCLDILRCINXQKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSLVGTLEQYKNPCLDILRCINXQKPLCPBEKQRHLD 127  
QY 121 KKQRFHNIRGRWTRGCMSCCRSRTRETOL 151  
DB 128 KKQRFHNIRGRWTRGCMSCCRSRTRETOL 158

#### RESULT 13

ID ADU66363 standard; protein; 158 AA.

XX ADU66363;

DT 10-FEB-2005 (first entry)

DE Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 4.

KW vaccine; MHC class I pathway; antigen specific immune response; tumor;

KM E7 protein; E6 protein.

OS Human papillomavirus type 16.

PN WO2004098526-A2.

PD 18-NOV-2004.

PF 05-MAY-2004; 2004WO-US013756.

PR 05-MAY-2003; 2003US-0467602P.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF;

DR WPI; 2004-813972/80.

PT New nucleic acid molecules encoding a fusion polypeptide comprising an  
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine  
PT for inducing or enhancing immune response or for inhibiting or preventing  
PT tumor growth.

PS Claim 11; SEQ ID NO 4; 67pp; English.

XX The invention comprises a nucleic acid molecule (DNA vaccine) that  
CC encodes a fusion polypeptide which is useful as a vaccine composition.  
CC The nucleic acid of the invention contains: a first nucleic acid encoding  
CC a polypeptide that promotes processing via the MHC class I pathway; a  
CC second sequence encoding a signal peptide; and a third sequence encoding  
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for  
CC inducing or enhancing an antigen specific immune response, or to inhibit  
CC growth or prevent re-growth of a tumor expressing Human papillomavirus  
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a  
CC human papillomavirus type 16 (HPV16) E6 protein of the invention.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 8; Length 158;  
Best Local Similarity 98.0%; Pred. No. 9.7e-84;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDFAFRDLCTIVRDGMPY 60  
 XX |||  
 Db 8 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDFAFRDLCTIVRDGMPY 67  
 QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCIINXQKPLCPBEKQRHLD 120  
 |||  
 Db 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLQOYNKPLCDLLIRCIINXQKPLCPBEKQRHLD 127  
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
 |||  
 Db 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158  
 RESULT 14  
 AEA40817 standard; protein, 158 AA.  
 XX AEA40817;  
 AC AEA40817;  
 DT 28-JUL-2005 (first entry)  
 XX  
 DE Anti-apoptotic vector HPV E6 antigenic protein, SEQ ID 7.  
 XX  
 KM immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;  
 KM vaccine; immune stimulation; tumor; cytostatic.  
 XX  
 OS Human papillomavirus - 16.  
 XX  
 PN W02005047501-A1.  
 XX  
 PD 26-MAY-2005.  
 XX  
 PF 24-FEB-2004; 2004MO-US005292.  
 XX  
 XX 24-FEB-2003; 2003US-0449429P.  
 PR 18-JUL-2003; 2003US-0488527P.  
 PR 31-DEC-2003; 2003US-0533792P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Wu T, Hung CF, Kim T;  
 PI  
 XX WPI; 2005-367009/37.  
 DR GENBANK; NC\_001526.  
 DR  
 PT New nucleic acid composition comprising a first nucleic acid vector  
 PT encoding an antigenic polypeptide and a second nucleic acid vector  
 PT inhibiting the growth of a tumor.  
 XX  
 PS Disclosure; SEQ ID NO 7; 158bp; English.  
 XX  
 CC The invention relates to a novel nucleic acid composition useful as an  
 CC immunogen. The composition comprises a combination of: a first nucleic  
 CC acid vector comprising a first sequence encoding an antigenic polypeptide  
 CC or peptide, and optionally, a second sequence linked to the first  
 CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);  
 CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.  
 CC When the second vector is administered with the first vector to a  
 CC subject, a T cell mediated immune response to the antigenic polypeptide  
 CC or peptide is induced that is greater in magnitude and/or duration than  
 CC an immune response induced by administration of the first vector alone.  
 CC The invention further includes: a particle comprising a material that is  
 CC suitable for introduction into a cell or an animal by particle  
 CC bombardment, bound to which is the first and second vectors or  
 CC composition; a pharmaceutical composition capable of inducing or  
 CC enhancing an antigen specific immune response, comprising the particle  
 CC and a carrier or an excipient; inducing or enhancing an antigen specific  
 CC immune response in a subject; increasing the numbers of CD8+ CTLs  
 CC specific for a selected desired antigen in a subject; and inhibiting the  
 CC growth of a tumor in a subject. The nucleic acid composition is useful as  
 CC an immunogen for inhibiting the growth of a tumor, hence it has  
 CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV

CC E6 antigenic protein of the invention.  
 XX  
 SQ Sequence 158 AA;  
 Query Match 99.2%; Score 823; DB 9; Length 158;  
 Best Local Similarity 98.0%; Pred. No. 9,76-84;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDFAFRDLCTIVRDGMPY 60  
 |||  
 Db 8 MFQDPQERPRKLPOLCTELQTTIHDIILECVYCKQQLRREYDFAFRDLCTIVRDGMPY 67  
 QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLLIRCIINXQKPLCPBEKQRHLD 120  
 |||  
 Db 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLQOYNKPLCDLLIRCIINXQKPLCPBEKQRHLD 127  
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151  
 |||  
 Db 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158  
 RESULT 15  
 AEA98532 standard; protein, 158 AA.  
 XX AEA98532;  
 AC AEA98532;  
 DT 08-SEP-2005 (first entry)  
 XX  
 DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 13.  
 XX  
 KM Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;  
 KM cancer; cervix tumor; cytostatic.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 PN US2005142541-A1.  
 XX  
 PD 30-JUN-2005.  
 XX  
 PF 23-DEC-2004; 2004US-00021949.  
 XX  
 PR 23-DEC-2003; 2003US-0532373P.  
 XX  
 PA (ARBO-) ARBOR VITA CORP.  
 XX  
 PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;  
 PI WPI; 2005-457781/46.  
 DR  
 PT New antibody composition comprising a mixture of monoclonal antibodies  
 PT for oncogenic strains of human papilloma virus, useful for diagnosing  
 PT cancer.  
 XX  
 PS Disclosure; SEQ ID NO 13; 161bp; English.  
 XX  
 CC The invention relates to an antibody composition comprising a mixture of  
 CC monoclonal antibodies that specifically bind to E6 proteins of human  
 CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one  
 CC of the monoclonal antibodies specifically binds to E6 proteins of at  
 CC least three different oncogenic HPV strains. Also included are a  
 CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,  
 CC comprising the antibody composition above), a method of detecting an HPV  
 CC E6 protein in a sample, a method of detecting the presence of an  
 CC oncogenic HPV E6 protein in a sample and a system for detecting the  
 CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a  
 CC first and a second binding partner for an oncogenic HPV E6 polypeptide,  
 CC where the first binding partner is a PDZ domain protein and the second  
 CC binding partner is an antibody that specifically binds to the E6 proteins  
 CC of at least three different oncogenic HPV strains). The antibody  
 CC composition, kit, methods, and system are useful for diagnosing cancer,  
 CC particularly cervical cancer. The present sequence is an HPV E6 protein.



**SQ** Sequence 158 AA;

Query Match	99.2%	Score 823	DB 9	Length 158
-------------	-------	-----------	------	------------

Best Local Similarity 98.0%; Pred. No. 9.7e-84;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MFQDQBSBPKLPOLCTELQTTIHDIILEFCYCKOOLLREYVDFAFRDLCIYRRGNPY	60
Db	8	MFQDQBSBPKLPOLCTELQTTIHDIILEFCYCKOOLLREYVDFAFRDLCIYRRGNPY	67
Qy	61	AVXDKCLFYSKISEYRHYCYSVGTTLEEQVYNKPLCDLLIRCTINQKPLCPBEKORHLD	120
Db	68	AVXDKCLFYSKISEYRHYCYSLYGTTLLEQVYNKPLCDLLIRCTINQKPLCPBEKORHLD	127
Qy	121	KKQRFHNIRGRWTGRCMSSCRSSRTTREFOL	151
Db	128	KKQRFHNIRGRWTGRCMSSCRSSRTTREFOL	158

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Job time : 223.345 secs

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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:11:25 ; Search time 44.2691 Seconds  
(without alignments)  
298.563 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830  
Sequence: 1 MFQDPQRRPRRLPQLCTELQ.....MTGRMGCRSSRRRTQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5.COMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6.COMB.pep:\*
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- 7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	162	1	US-08-316-239B-4
2	823	99.2	158	2	US-09-980-523A-2
3	823	99.2	158	3	US-09-763-616-1
4	823	99.2	162	1	US-08-316-239B-3
5	823	99.2	266	2	US-08-860-165-10
6	823	99.2	266	2	US-09-359-382-10
7	823	99.2	266	2	US-09-367-309A-1
8	823	99.2	273	2	US-09-485-885-4
9	823	99.2	292	2	US-09-485-885-10
10	823	99.2	371	2	US-09-485-885-6
11	823	99.2	390	2	US-09-485-885-14
12	818	98.6	151	2	US-09-701-080C-18
13	779.5	93.9	243	2	US-08-463-993-1
14	519	62.5	172	2	US-08-860-165-12
15	519	62.5	172	2	US-09-359-382-12
16	478	57.6	172	2	US-08-860-165-14
17	478	57.6	172	2	US-09-359-382-14
18	477	57.5	182	1	US-08-117-083-10
19	455.5	54.9	158	1	US-08-247-904B-10
20	455.5	54.9	171	2	US-08-767-942A-19
21	455.5	54.9	271	1	US-08-117-083-14
22	455.5	54.9	278	2	US-09-485-885-21
23	455.5	54.9	383	2	US-09-485-885-23
24	304	36.6	368	2	US-09-000-094-20
25	304	36.6	368	2	US-10-011-749-20
26	304	36.6	375	2	US-09-000-094-22

27	304	36.6	375	2	US-10-011-749-22	Sequence 22, Appl
28	304	36.6	465	2	US-09-000-094-24	Sequence 24, Appl
29	304	36.6	465	2	US-10-011-749-24	Sequence 24, Appl
30	304	36.6	1587	2	US-09-000-094-46	Sequence 46, Appl
31	304	36.6	1587	2	US-10-011-749-46	Sequence 46, Appl
32	163	19.6	30	1	US-08-363-586-4	Sequence 4, Appl
33	163	19.6	30	2	US-09-980-523A-4	Sequence 4, Appl
34	159	19.2	29	2	US-09-980-523A-8	Sequence 8, Appl
35	134.5	16.2	137	2	US-09-913-204-17	Sequence 17, Appl
36	130	15.7	22	2	US-09-980-523A-10	Sequence 10, Appl
37	128	15.4	23	2	US-09-601-729-276	Sequence 276, App
38	124	14.9	22	2	US-09-980-523A-6	Sequence 6, Appl
39	120	14.5	21	1	US-08-934-915-167	Sequence 167, App
40	119	14.3	137	2	US-09-913-204-3	Sequence 3, Appl
41	119	14.3	137	2	US-09-913-204-7	Sequence 7, Appl
42	119	14.3	137	2	US-09-913-204-13	Sequence 13, Appl
43	115	13.9	32	1	US-08-934-915-166	Sequence 166, App
44	115	13.9	32	1	US-08-466-285-2	Sequence 2, Appl
45	115	13.9	32	2	US-08-164-768-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-316-239B-4  
; Sequence 4, Application US/08316239B  
; Patent No. 5679509  
; GENERAL INFORMATION:  
; APPLICANT: Wheeler, Cosette M.  
; TITLE OF INVENTION: Methods and a Diagnostic Aid for  
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and  
; TITLE OF INVENTION: Cervical Cancer  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jagtiani & Associates  
; STREET: 6126 Rocky Way Court  
; CITY: Centreville  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 20120-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,239B  
; FILING DATE: 30-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jagtiani, Ajay A.  
; REGISTRATION NUMBER: 35,205  
; REFERENCE/DOCKET NUMBER: UNME-0001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 817-9453  
; TELEFAX: (703) 803-9387  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 162 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; US-08-316-239B-4  
Query Match 99.5%; Score 826; DB 1; Length 162;  
Best Local Similarity 98.7%; Pred. No. 8.2e-86;  
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVDFAFRDLCTIVRDGNPY 60
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|
Db 8 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVDFAFRDLCTIVRDGNPY 67
|
|
|
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRCNXQKPLCPBEKQRHLD 120
|
|
|
Db 68 AVCDCKLFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRCNXQKPLCPBEKQRHLD 127
|
|
|
Qy 121 KKQRFNIRGRWTCRMSCCRSSRTRRETOL 151
|
|
|
Db 128 KKQRFNIRGRWTCRMSCCRSSRTRRETOL 158
|
|
|
RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOIPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIS, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980, 523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
Query Match 99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.7e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVDFAFRDLCTIVRDGNPY 60
|
|
|
Db 8 MFODPQERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVDFAFRDLCTIVRDGNPY 67
|
|
|
Qy 61 AVXDCKLFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRCNXQKPLCPBEKQRHLD 120
|
|
|
Db 68 AVCDCKLFYSKISEYRHVCYSVGTTLLEQYNNKPLCDLLIRCNXQKPLCPBEKQRHLD 127
|
|
|
Qy 121 KKQRFNIRGRWTCRMSCCRSSRTRRETOL 151
|
|
|
Db 128 KKQRFNIRGRWTCRMSCCRSSRTRRETOL 158
|
|
|
RESULT 4
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmeter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: AU P01645/99
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: AU P5733/98
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-763-616-1
Query Match 99.2%; Score 823; DB 3; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.7e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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US-08-316-239B-3

Query Match 99.2%; Score 823; DB 1; Length 162;  
Best Local Similarity 98.0%; Pred. No. 1.8e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 127  
QY 121 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 151  
DB 128 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 158

RESULT 5  
US-08-860-165-10  
Sequence 10, Application US/08860165A  
Patent No. 6004557  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scitling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
CURRENT FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU P0157  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-10

Query Match 99.2%; Score 823; DB 2; Length 266;  
Best Local Similarity 98.0%; Pred. No. 3.2e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 127  
QY 121 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 151  
DB 128 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 158

RESULT 6  
US-09-359-382-10  
Sequence 10, Application US/09359382  
Patent No. 6306397  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, Scitling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
CURRENT FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU P0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-10

Query Match 99.2%; Score 823; DB 2; Length 266;  
Best Local Similarity 98.0%; Pred. No. 3.2e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 127  
QY 121 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 151  
DB 128 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 158

RESULT 7  
US-09-367-309A-1  
Sequence 1, Application US/09367309A  
Patent No. 6428807  
GENERAL INFORMATION:  
APPLICANT: MACFARLAN, RODERICK I.  
APPLICANT: MALLIAROS, JIM  
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES  
FILE REFERENCE: 017227/0149  
CURRENT APPLICATION NUMBER: US/09/367,309A  
CURRENT FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: PCT/AU98/00080  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: AU PO 5178  
PRIOR FILING DATE: 1997-02-19  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 2; Length 266;  
Best Local Similarity 98.0%; Pred. No. 3.2e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 60  
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDFAFRDLCTIVRDGPNY 67  
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 120  
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRCNXOKPLCPBEKQRHLD 127  
QY 121 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 151  
DB 128 KKORFHNIRGWRGCMSCCRSSRTTRRETOL 158

RESULT 8  
US-09-485-885-4  
Sequence 4, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Bernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-4

Query Match 99.2%; Score 823; DB 2; Length 273;  
Best Local Similarity 98.0%; Pred. No. 3.3e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 60  
Db 114 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 173  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120  
Db 174 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 233  
Qy 121 KKORFHNIRGRWTRCSCCRSSRTRETOL 151  
Db 234 KKORFHNIRGRWTRCSCCRSSRTRETOL 264

RESULT 9  
US-09-485-885-10  
Sequence 10, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Bernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 10  
LENGTH: 292  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-10

Query Match 99.2%; Score 823; DB 2; Length 292;  
Best Local Similarity 98.0%; Pred. No. 3.6e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 60  
Db 133 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 192  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120  
Db 193 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 252  
Qy 121 KKORFHNIRGRWTRCSCCRSSRTRETOL 151  
Db 253 KKORFHNIRGRWTRCSCCRSSRTRETOL 283

RESULT 10  
US-09-485-885-6  
Sequence 6, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Bernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: GB 9717953.5  
PRIOR FILING DATE: 1997-08-22  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 6  
LENGTH: 371  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-485-885-6

Query Match 99.2%; Score 823; DB 2; Length 371;  
Best Local Similarity 98.0%; Pred. No. 4.8e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 60  
Db 114 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLLRREYVDFARFDCIYVRDGNPY 173  
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 120  
Db 174 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRICINXOKPLCPBEKORHLD 233  
Qy 121 KKORFHNIRGRWTRCSCCRSSRTRETOL 151  
Db 234 KKORFHNIRGRWTRCSCCRSSRTRETOL 264

RESULT 11  
US-09-485-885-14  
Sequence 14, Application US/09485885  
Patent No. 6342224  
GENERAL INFORMATION:  
APPLICANT: Bruck, Claudine  
APPLICANT: Cabezon Silva, Teresa  
APPLICANT: Delisse, Anne-Marie Eva Bernande  
APPLICANT: Gerard, Catherine Marie Ghislaine  
APPLICANT: Lombardo-Bencheikh, Angela  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45107  
CURRENT APPLICATION NUMBER: US/09/485,885  
PRIOR FILING DATE: 2000-02-18  
PRIOR APPLICATION NUMBER: PCT/EP98/05285  
PRIOR FILING DATE: 1998-08-17

;; PRIOR APPLICATION NUMBER: GB 9717953.5  
;; PRIOR FILING DATE: 1997-08-22  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: FASTSEQ for Windows Version 3.0  
;; SEQ ID NO 14  
;; LENGTH: 390  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
US-09-485-885-14

Query Match 99.2%; Score 823; DB 2; Length 390;  
Best Local Similarity 98.0%; Pred. No. 5,1e-85;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60  
DB 133 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 192  
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120  
DB 193 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 252  
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151  
DB 253 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 283

RESULT 12  
US-09-701-080C-18  
;; Sequence 18, Application US/09701080C  
;; Patent No. 6864054

;; GENERAL INFORMATION:  
;; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY  
;; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F  
;; FILE REFERENCE: N73477C GCM  
;; CURRENT APPLICATION NUMBER: US/09/701,080C  
;; PRIOR FILING DATE: 2001-02-27  
;; PRIOR APPLICATION NUMBER: GB 9811303.8  
;; PRIOR FILING DATE: 1998-05-26  
;; PRIOR APPLICATION NUMBER: GB 9900157.0  
;; PRIOR FILING DATE: 1999-01-05  
;; NUMBER OF SEQ ID NOS: 36  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 18  
;; LENGTH: 151  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus  
US-09-701-080C-18

Query Match 98.6%; Score 818; DB 2; Length 151;  
Best Local Similarity 97.4%; Pred. No. 6,1e-85;  
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60  
DB 1 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60  
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120  
DB 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120  
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151  
DB 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151

RESULT 13  
US-09-462-993-1  
;; Sequence 1, Application US/09462993  
;; Patent No. 6884786  
;; GENERAL INFORMATION:  
;; APPLICANT: KIEVY, Marie-Paule

;; APPLICANT: BAILOU, Jean-Marc  
;; APPLICANT: BIZOUARNE, Nadine  
;; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC  
;; TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION  
;; FILE REFERENCE: 01753-122  
;; CURRENT APPLICATION NUMBER: US/09/462,993  
;; PRIOR FILING DATE: 2000-04-17  
;; PRIOR APPLICATION NUMBER: PCT/FR98/01576  
;; PRIOR FILING DATE: 1998-07-17  
;; PRIOR APPLICATION NUMBER: FR 97/09152  
;; PRIOR FILING DATE: 1997-07-18  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: Patentin Ver. 2.2  
;; SEQ ID NO 1  
;; LENGTH: 243  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Derived from  
;; OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein  
;; OTHER INFORMATION: fused F protein signals, clone B6\*TWf.  
US-09-462-993-1

Query Match 93.9%; Score 779.5; DB 2; Length 243;  
Best Local Similarity 94.7%; Pred. No. 2,5e-80;  
Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 1 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60  
DB 36 MFODPOEPRRLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 95  
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 120  
DB 96 AVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 150  
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151  
DB 151 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 181

RESULT 14  
US-08-860-165-12  
;; Sequence 12, Application US/08860165A  
;; Patent No. 6004557

;; GENERAL INFORMATION:  
;; APPLICANT: EDWARDS, Scirling John  
;; APPLICANT: COX, John Cooper  
;; APPLICANT: WEBB, Elizabeth Ann  
;; APPLICANT: FRASER, Ian  
;; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
;; FILE REFERENCE: 17227/130  
;; CURRENT APPLICATION NUMBER: US/08/860,165A  
;; PRIOR FILING DATE: 1997-09-22  
;; EARLIER APPLICATION NUMBER: PCT/AU95/00868  
;; EARLIER FILING DATE: 1995-12-20  
;; EARLIER APPLICATION NUMBER: AU EN0157  
;; EARLIER FILING DATE: 1994-12-20  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: Patentin Ver. 2.0  
;; SEQ ID NO 12  
;; LENGTH: 172  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-12

Query Match 62.5%; Score 519; DB 2; Length 172;  
Best Local Similarity 96.8%; Pred. No. 5,7e-51;  
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPFAVXDCKLFYSKISSEYRHVCYSVGTTLBQOYNKPLCDLLIRICINXQKPLCEEKQRHLD 116

Db 2 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTLLBEOYNNKPLCDLLIRCIHQKPLCPBEKQ 61

QY 117 RHLDKQRFHNIRGRMTGRCMSCCRSSRTRETQL 151

Db 62 RHLDKQRFHNIRGRMTGRCMSCCRSSRTRETQL 96

## RESULT 15

US-09-359-382-12

; Sequence 12, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 017227/0148

; CURRENT APPLICATION NUMBER: US/09/359,382

; EARLIER FILING DATE: 1999-07-23

; EARLIER APPLICATION NUMBER: US 08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-359-382-12

Query Match 62.5%; Score 519; DB 2; Length 172;

Best Local Similarity 96.8%; Pred. No. 5.7e-51;

Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTLLBEOYNNKPLCDLLIRCIHQKPLCPBEKQ 116

Db 2 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTLLBEOYNNKPLCDLLIRCIHQKPLCPBEKQ 61

QY 117 RHLDKQRFHNIRGRMTGRCMSCCRSSRTRETQL 151

Db 62 RHLDKQRFHNIRGRMTGRCMSCCRSSRTRETQL 96

Search completed: June 6, 2006, 12:13:14

Job time : 45.2691 secs



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:10 ; Search time 164.341 Seconds  
(without alignments)  
425.611 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830  
Sequence: 1 MFQDPQERPRKLPOLCTELQ.....WTGRCMSCCSSRTRRETOL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications MA Main.\*

- 1: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US10\_PUBCOMB.pep:\*
- 6: /EMC\_Ceiera\_SIDS3/ptodara/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	828	99.8	248	5	US-10-530-253-3
2	828	99.8	248	5	US-10-530-253-5
3	826	99.5	151	5	US-10-484-063-20
4	826	99.5	151	5	US-10-484-063-27
5	826	99.5	151	5	US-10-530-253-13
6	826	99.5	248	5	US-10-530-253-11
7	823	99.2	158	5	US-10-858-384-2
8	823	99.2	158	5	US-10-367-057-16
9	823	99.2	158	6	US-11-021-949-13
10	823	99.2	158	6	US-11-021-949-13
11	823	99.2	171	4	US-10-472-724-2
12	823	99.2	248	5	US-10-530-253-9
13	823	99.2	248	5	US-10-530-253-11
14	823	99.2	256	6	US-11-192-923A-2
15	823	99.2	266	3	US-09-367-309A-1
16	823	99.2	273	4	US-10-000-903-4
17	823	99.2	273	5	US-10-899-771-4
18	823	99.2	292	4	US-10-000-903-10
19	823	99.2	292	5	US-10-899-771-10
20	823	99.2	371	4	US-10-000-903-6
21	823	99.2	371	5	US-10-899-771-6
22	823	99.2	390	4	US-10-000-903-14
23	823	99.2	390	5	US-10-899-771-14
24	821	98.9	248	5	US-10-530-253-7
25	819	98.7	151	4	US-10-177-390-6
26	779.5	93.9	243	6	US-11-072-288-1
27	578	69.6	149	5	US-10-530-253-18

28	578	69.6	149	6	US-11-021-949-14	Sequence 14, Appl
29	523	63.0	149	5	US-10-530-253-16	Sequence 16, Appl
30	523	63.0	149	6	US-11-021-949-18	Sequence 18, Appl
31	520	62.7	149	5	US-10-530-253-17	Sequence 17, Appl
32	520	62.7	149	6	US-11-021-949-16	Sequence 16, Appl
33	498	60.0	149	6	US-11-021-949-160	Sequence 360, App
34	496	59.8	149	5	US-10-530-253-24	Sequence 24, Appl
35	496	59.8	149	6	US-11-021-949-15	Sequence 15, Appl
36	487	58.7	148	6	US-10-530-253-22	Sequence 22, Appl
37	487	58.7	148	6	US-11-021-949-17	Sequence 17, Appl
38	484	58.3	148	6	US-11-021-949-359	Sequence 359, App
39	483	58.2	148	6	US-11-021-949-19	Sequence 19, Appl
40	468.5	56.4	158	6	US-10-530-253-26	Sequence 26, Appl
41	468.5	56.4	158	6	US-11-021-949-361	Sequence 361, App
42	460	55.4	151	5	US-10-530-253-21	Sequence 21, Appl
43	460	55.4	151	6	US-11-021-949-24	Sequence 24, Appl
44	459.5	55.4	158	5	US-10-530-253-20	Sequence 20, Appl
45	459.5	55.4	158	6	US-11-021-949-29	Sequence 29, Appl

ALIGNMENTS

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RESULT 1
US-10-530-253-3
; Sequence 3, Application US/10530253
; Publication No. US20060014926a1
; GENERAL INFORMATION:
; APPLICANT: Casacti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530.253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-3
Query Match 99.8%; Score 828; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 6.5e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRRVDFAFADLCTIVRDGMPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRRVDFAFADLCTIVRDGMPY 60
QY 61 AVXDKCIKFYSKISEYRHYCYSVYGTTLBQYKPLCDLLIRCIKXQKPLCEPKORHLD 120
DB 61 AVXDKCIKFYSKISEYRHYCYSVYGTTLBQYKPLCDLLIRCIKXQKPLCEPKORHLD 120
QY 121 KKQRFHNRIGWTRGCMSCCSSRTRRETOL 151
DB 121 KKQRFHNRIGWTRGCMSCCSSRTRRETOL 151
QY 121 KKQRFHNRIGWTRGCMSCCSSRTRRETOL 151
DB 121 KKQRFHNRIGWTRGCMSCCSSRTRRETOL 151
RESULT 2
US-10-530-253-5
; Sequence 5, Application US/10530253
; Publication No. US20060014926a1
; GENERAL INFORMATION:
; APPLICANT: Casacti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
```

```

; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530, 253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-5

Query Match          99.8%; Score 828; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
QY 61 AVXDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
DB 61 AVGDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151
DB 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151

RESULT 3
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
QY 61 AVXDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
DB 61 AVCDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151
DB 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151
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DB 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151

RESULT 4
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYVDFAFRDLCIVRDGPNY 60
QY 61 AVXDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
DB 61 AVCDCKLKFYSKISEYRHYCVSVGTTLEQOYNKPLCDLLIRCTNXOKPLCPBEKQRLHD 120
QY 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151
DB 121 KKQRFHNIRGWTGRCMSCCSSRTRRETOL 151

RESULT 5
US-10-530-253-13
; Sequence 13, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-13

Query Match          99.5%; Score 826; DB 5; Length 151;
Best Local Similarity 98.7%; Pred. No. 6e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
DB      1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
QY      61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB      61 AVCDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
QY      121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB      121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 6
US-10-530-253-1
; Sequence 1, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-1

Query Match      99.5%; Score 826; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 1,1e-80;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
DB      1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
QY      61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB      61 AVCDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
QY      121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB      121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLAD, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR APPLICATION NUMBER: FR 9907012
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;; PRIOR FILING DATE: 1999-06-03
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: Patent Ver. 3.2
;; SEQ ID NO 2
;; LENGTH: 158
;; TYPE: PRT
;; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      99.2%; Score 823; DB 5; Length 158;
Best Local Similarity 98.0%; Pred. No. 1,3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
DB      8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
QY      61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB      68 AVCDCKLKFYSKISEYRHYCYSLVGTLEQYNNKPLCDLLIRCTINXOKPLCPBEKQRHLD 127
QY      121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB      128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 9
US-11-021-949-13
; Sequence 13, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID
```

```
; APPLICANT: BELMARES, MICHAEL P
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-13
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Query Match          99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 120
Db 68 AVCDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 127
Qy 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
Db 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158
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RESULT 10
US-11-206-138-3
; Sequence 3, Application US/11206138
; Publication No. US2006003919A1
; GENERAL INFORMATION:
; APPLICANT: Healthbanc Biotech CO. LTD.
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer
; FILE REFERENCE: P7819/0613
; CURRENT APPLICATION NUMBER: US/11/206,138
; CURRENT FILING DATE: 2005-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-11-206-138-3
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Query Match          99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 120
Db 68 AVCDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 127
Qy 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
Db 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158
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RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
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; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
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Query Match          99.2%; Score 823; DB 4; Length 171;
Best Local Similarity 98.0%; Pred. No. 1.5e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 13 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 72
Qy 61 AVXDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 120
Db 73 AVCDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 132
Qy 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
Db 133 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 163
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RESULT 12
US-10-530-253-9
; Sequence 9, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-9
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Query Match          99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2.2e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 FODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 61
Db 99 FODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 158
Qy 62 VXDCKLKFYSKISEYRHVCYSVYGTTLLEQOYNKPLCDLLIRCNXQKPLCPBEKQRLHD 121
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Db 159 VGDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLDK 218  
Qy 122 KORFHNIRGRWTCRMSCCRSSRTRETOL 151  
Db 219 KORFHNIRGRWTCRMSCCRSSRTRETOL 248

RESULT 13  
US-10-530-253-11  
; Sequence 11, Application US/10530253  
; Publication No. US20060014926A1  
; GENERAL INFORMATION:  
; APPLICANT: Cassecci, Maria C.  
; APPLICANT: Smith, Larry  
; APPLICANT: Jeffrey K. Pullen  
; APPLICANT: Susan P. McElhinney  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 00630/100M137-US2  
; CURRENT APPLICATION NUMBER: US/10/530,253  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
; PRIOR FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 60/415,929  
; PRIOR FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-10-530-253-11

Query Match 99.2%; Score 823; DB 5; Length 248;  
Best Local Similarity 98.7%; Pred. No. 2.2e-80;  
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPYA 61  
Db 99 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPYA 158  
Qy 62 VXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLDK 121  
Db 159 VGDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLDK 218  
Qy 122 KORFHNIRGRWTCRMSCCRSSRTRETOL 151  
Db 219 KORFHNIRGRWTCRMSCCRSSRTRETOL 248

RESULT 14  
US-11-192-923A-2  
; Sequence 2, Application US/11192923A  
; Publication No. US20060018928A1  
; GENERAL INFORMATION:  
; APPLICANT: PANQ, XIAOWU  
; TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS  
; FILE REFERENCE: 116620-003  
; CURRENT APPLICATION NUMBER: US/11/192,923A  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: CN 03115272.4  
; PRIOR FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: CN 03115273.2  
; PRIOR FILING DATE: 2003-01-30  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 2  
; LENGTH: 256  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-11-192-923A-2

Query Match 99.2%; Score 823; DB 6; Length 256;  
Best Local Similarity 98.0%; Pred. No. 2.3e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60  
Db 106 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 165  
Qy 61 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLD 120  
Db 166 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLD 225  
Qy 121 KORFHNIRGRWTCRMSCCRSSRTRETOL 151  
Db 226 KORFHNIRGRWTCRMSCCRSSRTRETOL 256

RESULT 15  
US-09-367-309A-1  
; Sequence 1, Application US/09367309A  
; Publication No. US20020081329A1  
; GENERAL INFORMATION:  
; APPLICANT: MACFARLAN, RODERICK I.  
; APPLICANT: MALLIAROS, JIM  
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES  
; FILE REFERENCE: 017227/0149  
; CURRENT APPLICATION NUMBER: US/09/367,309A  
; CURRENT FILING DATE: 1999-08-11  
; PRIOR APPLICATION NUMBER: PCT/AU98/00080  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: AU PO 5178  
; PRIOR FILING DATE: 1997-02-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 266  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 3; Length 266;  
Best Local Similarity 98.0%; Pred. No. 2.4e-80;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFRDLCTIVRDGNPY 67  
Qy 61 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLD 120  
Db 68 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNNKPLCDLLIRINCQKPLCPBEKORHLD 127  
Qy 121 KORFHNIRGRWTCRMSCCRSSRTRETOL 151  
Db 128 KORFHNIRGRWTCRMSCCRSSRTRETOL 158

Search completed: June 6, 2006, 12:32:59  
Job time : 164.341 secs

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## OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:35 ; Search time 10.9157 Seconds

(without alignments)  
159.985 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830  
Sequence: 1 MFQDPQRPRKRLPOLCTELQ.....MTGRCMSCCRSRRTREQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_NEW\_PUB pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US06\_NEW\_PUB pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US07\_NEW\_PUB pep:\*  
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8: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US00\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	114	13.7	US-11-209-206-4	Sequence 4, Appli
2	74.5	9.0	US-11-223-610-1	Sequence 1, Appli
3	74.5	9.0	US-10-953-854-4	Sequence 4, Appli
4	74.5	9.0	US-10-953-854-6	Sequence 6, Appli
5	74.5	9.0	US-10-953-854-2	Sequence 2, Appli
6	72.5	8.7	US-10-953-349-33871	Sequence 33871, A
7	72.5	8.7	US-10-953-349-33870	Sequence 33870, A
8	72.5	8.7	US-10-953-349-33869	Sequence 33869, A
9	71	8.6	US-11-293-697-2762	Sequence 2762, Ap
10	68	8.2	US-11-209-206-5	Sequence 5, Appli
11	65	7.8	US-10-953-349-17182	Sequence 17182, A
12	63.5	7.7	US-10-953-349-6306	Sequence 6306, Ap
13	63.5	7.7	US-10-953-349-6305	Sequence 6305, Ap
14	63.5	7.7	US-10-953-349-6304	Sequence 6304, Ap
15	63	7.6	US-10-953-349-32521	Sequence 32521, A
16	63	7.6	US-10-953-349-32520	Sequence 32520, A
17	63	7.6	US-10-953-349-32519	Sequence 32519, A
18	62.5	7.5	US-11-293-697-4876	Sequence 4876, Ap
19	62.5	7.5	US-11-106-014-8	Sequence 8, Appli
20	62	7.5	US-10-196-749-474	Sequence 474, App
21	62	7.5	US-10-505-928-225	Sequence 225, App
22	61.5	7.4	US-10-953-349-18091	Sequence 18091, A
23	61.5	7.4	US-10-953-349-18090	Sequence 18090, A
24	61.5	7.4	US-10-953-349-18089	Sequence 18089, A
25	61.5	7.4	US-11-293-697-4346	Sequence 4346, Ap

26	61	7.3	259	6	US-10-953-349-19918	Sequence 19918, A
27	61	7.3	355	6	US-10-953-349-19917	Sequence 19917, A
28	60.5	7.3	267	6	US-10-953-349-28497	Sequence 28497, A
29	60.5	7.3	314	6	US-10-538-066-365	Sequence 365, App
30	60.5	7.3	706	7	US-11-293-697-3919	Sequence 3919, App
31	60.5	7.3	971	6	US-10-505-928-397	Sequence 397, App
32	60.5	7.3	1085	6	US-10-505-928-175	Sequence 175, App
33	60	7.2	867	7	US-11-293-697-1034	Sequence 3034, App
34	59	7.1	233	6	US-10-953-349-13389	Sequence 13389, A
35	59	7.1	258	6	US-10-953-349-1032	Sequence 1032, App
36	59	7.1	369	6	US-10-953-349-1031	Sequence 1031, App
37	59	7.1	376	6	US-10-953-349-1030	Sequence 1030, App
38	59	7.1	385	6	US-10-953-349-13388	Sequence 13388, A
39	59	7.1	400	6	US-10-953-349-13387	Sequence 13387, A
40	59	7.1	428	6	US-10-953-349-25008	Sequence 25008, A
41	59	7.1	433	6	US-10-953-349-25007	Sequence 25007, A
42	59	7.1	436	6	US-10-953-349-25006	Sequence 25006, A
43	58.5	7.0	204	6	US-10-953-349-37463	Sequence 37463, A
44	58.5	7.0	251	6	US-10-953-349-38140	Sequence 38140, A
45	58.5	7.0	280	6	US-10-953-349-38139	Sequence 38139, A

## ALIGNMENTS

RESULT 1  
US-11-209-206-4  
Sequence 4, Application US/11209206  
Publication No. US20060110794A1  
GENERAL INFORMATION:  
APPLICANT: Impact Diagnostics  
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus  
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi  
TITLE OF INVENTION: Associated Cancers  
FILE REFERENCE: 3352-2-2  
CURRENT APPLICATION NUMBER: US/11/209, 206  
CURRENT FILING DATE: 2005-08-22  
PRIOR APPLICATION NUMBER: US 60/394, 172  
PRIOR FILING DATE: 2002-07-02  
PRIOR APPLICATION NUMBER: US 09/828, 645  
PRIOR FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Derived from the E6 early coding region of HPV 16  
US-11-209-206-4  
Query Match 13.7%; Score 114; DB 7; Length 22;  
Best Local Similarity 95.5%; Pred. No. 3.7e-06;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 55 RDGNPVAVXDCKLKFYSKISEY 76  
Db 1 RDGNPVAVCDCKLKFYSKISEY 22  
RESULT 2  
US-11-223-610-1  
Sequence 1, Application US/11223610  
Publication No. US20060111289A1  
GENERAL INFORMATION:  
APPLICANT: Miziejewski, Gerald J.  
TITLE OF INVENTION: Compositions and Methods of Using Alpha-Fetoprotein Growth  
TITLE OF INVENTION: Inhibitory Peptides  
FILE REFERENCE: HOLLAND-09516  
CURRENT APPLICATION NUMBER: US/11/223, 610  
CURRENT FILING DATE: 2005-09-09  
NUMBER OF SEQ ID NOS: 181





US-10-933-854-2

Query Match 9.0%; Score 74.5; DB 6; Length 609;  
Best Local Similarity 23.4%; Pred. No. 1.7;  
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

QY 6 QERPRRLPOLCTELQTTIHDIILCEVCYCKQQQLRREVDFAFRDLCTIVY----- 54  
DB 279 ODGEKIMSYICSQ-ODTISNKTIEC-CKLTLE-----RGQCIIHAENDEKPEGLS 327  
QY 55 -----RDGNPYAVXDKCLKFYSKISEY--RHVCYSVGTTLTLEQQYNKPLCDLLIRC 103  
DB 328 PNLNRFLDDRDFQNGSSGSEKQNIPLASFVHEYSRRHRLQPLAV---SVILVAKCYQDLLEKC 384  
QY 104 INXQKPL-C-----PEEKORHLDDKQ 123  
DB 385 FQTEPNLECCODKGEELQKYOIESQ 409

RESULT 6

US-10-953-349-33871  
; Sequence 33871, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33871  
; LENGTH: 800  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33871

Query Match 8.7%; Score 72.5; DB 6; Length 800;  
Best Local Similarity 23.3%; Pred. No. 3.8;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQGRPRRLPOLCTELQTTIHDIILCEVCYCKQQ-----LRRREVY----DFAFRDLCTIVY 54  
DB 460 DDNADPSPKSKSCNESRVTVERNLQTPPKQSHMVSTSLAKCHPLOSTFASPTVC--- 516  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLTLEQQ- 91  
DB 517 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYVNFKQILBQQT 573  
QY 92 ---YNKPLCDLLIRCINXQKPLCPBE 114  
DB 574 TLFENRHIDQLILCLCYGVAKVCOLE 599

RESULT 7

US-10-953-349-33870  
; Sequence 33870, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33870  
; LENGTH: 809  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33870

Query Match 8.7%; Score 72.5; DB 6; Length 809;  
Best Local Similarity 23.3%; Pred. No. 3.8;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQGRPRRLPOLCTELQTTIHDIILCEVCYCKQQ-----LRRREVY----DFAFRDLCTIVY 54  
DB 469 DDNADPSPKSKSCNESRVTVERNLQTPPKQSHMVSTSLAKCHPLOSTFASPTVC--- 525  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLTLEQQ- 91  
DB 526 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYVNFKQILBQQT 582  
QY 92 ---YNKPLCDLLIRCINXQKPLCPBE 114  
DB 583 TLFENRHIDQLILCLCYGVAKVCOLE 608

RESULT 8

US-10-953-349-33869  
; Sequence 33869, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 33869  
; LENGTH: 867  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
US-10-953-349-33869

Query Match 8.7%; Score 72.5; DB 6; Length 867;  
Best Local Similarity 23.3%; Pred. No. 4.1;  
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQGRPRRLPOLCTELQTTIHDIILCEVCYCKQQ-----LRRREVY----DFAFRDLCTIVY 54  
DB 527 DDNADPSPKSKSCNESRVTVERNLQTPPKQSHMVSTSLAKCHPLOSTFASPTVC--- 583  
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLTLEQQ- 91  
DB 584 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYVNFKQILBQQT 640  
QY 92 ---YNKPLCDLLIRCINXQKPLCPBE 114  
DB 641 TLFENRHIDQLILCLCYGVAKVCOLE 666

RESULT 9

US-11-293-697-2762  
; Sequence 2762, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NOVEL FULL LENGTH CDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2762  
; LENGTH: 531  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-2762

Query Match 8.6%; Score 71; DB 7; Length 531;  
Best Local Similarity 22.0%; Pred. No. 3.5;  
Matches 28; Conservative 16; Mismatches 55; Indels 28; Gaps 5;  
Qy 28 LECVCKO--OLLRREYVDFAFRDLCTIVRDGNPYAVXDKCLKFYSKISEYRHVCYSYVG 85  
Db 175 LGCKCKSCGCLTNAE-----YISKDGLPYCEADYNAKGIKDCSCBK----ITG 221  
Qy 86 TLE--QQYNKPLCDLLIRCIKXOKPLCPBEKQRLDKQRFHNIKRGWTCRSCSCSS 143  
Db 222 RVLAGEKHYPSCALCVGC-----GQMFAGEEMVLOQSSIMHPACROAARTE 270  
Qy 144 RTRETO 150  
Db 271 DRNKEIR 277

RESULT 10  
US-11-209-206-5  
; Sequence 5, Application US/11209206  
; Publication No. US2006010794A1  
; GENERAL INFORMATION:  
; APPLICANT: Impact Diagnostics  
; TITLE OF INVENTION: Impact Diagnostics  
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus  
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil  
; TITLE OF INVENTION: Associated Cancers  
; FILE REFERENCE: 3352-2-2  
; CURRENT APPLICATION NUMBER: US/11/209,206  
; CURRENT FILING DATE: 2005-08-22  
; PRIOR APPLICATION NUMBER: US 60/394,172  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US 09/828,645  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 18  
US-11-209-206-5

Query Match 8.2%; Score 68; DB 7; Length 22;  
Best Local Similarity 61.9%; Pred. No. 0.23;  
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
Qy 65 KCLKFYSKISEYRHVCYSYVG 85  
Db 1 KCIDFGSKIRLRHYSDSYVG 21

RESULT 11  
US-10-953-349-17182  
; Sequence 17182, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERAPY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17182  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-17182

Query Match 7.8%; Score 65; DB 6; Length 369;  
Best Local Similarity 22.2%; Pred. No. 9.9;  
Matches 39; Conservative 24; Mismatches 59; Indels 54; Gaps 10;  
Qy 1 MFQDQERPRKLPOLCTELQTTIHDIILBCVCKQOLL-----RRE-- 41  
Db 62 LKSPFLRP-----LFIAASGIPFIVITELYSYDPLMWKVDGQNSLFHAIWMRQEKI 116  
Qy 42 ---VYDF-ARFDLCIVRDGNPYAVXDKCLKFYSKI--SEYRHVCYSYVGTLEQYN-- 93  
Db 117 FNLIVDIGAKHDLTTSYRDNNNNHNI-----LHLAKKLAPSSQLHY--VSGAALOMORELL 169  
Qy 94 -----KPLCDLLIRCIKXOKPLCP-----EKORHLDKQRFHNIKRGWTCRSCSCC 140  
Db 170 WFKVEVKIQLPKEIKDSQGRTPQMLFTBEHKELAKEG-----KMLKNTASSC 219

RESULT 12  
US-10-953-349-6306  
; Sequence 6306, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERAPY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6306  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6306

Query Match 7.7%; Score 63.5; DB 6; Length 419;  
Best Local Similarity 21.0%; Pred. No. 16;  
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;  
Qy 7 ERPRKLPOLCTELQTTIHDIILBCVCKQOLLREV-----YDFAFRD 49  
Db 194 ESVHKIDNVGSIYTHIPIIAPKVHVAAYFNKHTERNOKTSYITQGVNADGIFTD 253  
Qy 50 LCTIVRDGNPYAVXDKCLKFYSKISEYRHVCYSYVGTLEQYNKPLCDLLIRCIKXOKP 109  
Db 254 VCI---GNPGLSTDGDIKSSLSRQARAGMLRDSWIVNGSGLPDLTYL----- 300  
Qy 110 LCPBEKQ-----RHLDDKQ-----RFHNIKRGWTCRSCSCSRTRRETO 150  
Db 301 LVPTTRONLTWTOAFAFMSIGETIGIATAFAERLKGW-----ACIQKRTBVVLQ 350

RESULT 13  
US-10-953-349-6305  
; Sequence 6305, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERAPY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6305  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6305

Query Match 7.7%; Score 63.5; DB 6; Length 515;



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A:Note: host Homo sapiens (man)

A;Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C/Accession: E40824; S36521  
R/Marich, J.E.; Pontier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virology 186; 770-776, 1992  
A/Title: The phylogenetic relationship and complete nucleotide sequence of human papilloma virus  
A/Reference number: A40824; MUID:92124753; PMID:1310198  
A/Accession: E40824  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-149 <MAR>  
A/Cross-references: UNIPROT:P27228; UNIPARC:UPI00001383CF; GB:M74117; NID:G333050; PIDN:  
R/Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36521  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-149 <DEL>  
A/Cross-references: UNIPARC:UPI00001383CF; EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PI  
A/Experimental source: strain 35H  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F/30-66/Region: zinc finger CCCC motif  
F/103-139/Region: zinc finger CCCC motif

Query Match 69.6%; Score 578; DB 1; Length 149;  
Best Local Similarity 71.5%; Pred. No. 5.7e-48;  
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTTHDILIECVYCKQQLLRREYDFAFADLCIYVRDGNPY 60  
DB 1 MFODPARPRYKHLCLCHEVESIHETCLANCYCKQELORSSEYDFACDLCIYVRREGQPY 60  
QY 61 AYXDKCLKFSKISEYRHVCYSYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 GVCKCLKFSKISEYRWYRSYVGETLEKQCNKQLCHLLIRCTCQKPLCPVEKQRHLE 120  
QY 121 KQRFNIRGRWTRCSCCRSSRTRETQL 151  
DB 121 EKKRFNIGRWTRCSCCRSRTRETQV 149

## RESULT 3

W6WL31  
E6 protein - human papillomavirus type 31  
C/Species: human papillomavirus type 31  
A/Note: host Homo sapiens (man)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C/Accession: A32444  
R/Goldborough, M.D.; Dislyvestre, D.; Temple, G.F.; Lorincz, A.T.  
Virology 171; 306-311, 1989  
A/Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ  
A/Reference number: A94398; MUID:89299478; PMID:2545036  
A/Accession: A32444  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-149 <GOL>  
A/Cross-references: UNIPROT:P17386; UNIPARC:UPI00001383CB; GB:J04353; NID:G333048; PIDN:  
C/Comment: This protein may be involved in the oncogenic potential of this virus.  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F/30-66/Region: zinc finger CCCC motif  
F/103-139/Region: zinc finger CCCC motif

Query Match 63.0%; Score 523; DB 1; Length 149;  
Best Local Similarity 64.9%; Pred. No. 9.9e-43;  
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTTHDILIECVYCKQQLLRREYDFAFADLCIYVRDGNPY 60  
DB 1 MFKNPARPRKHLCLCHEVESIHETCLANCYCKQELORSSEYDFAFADLCIYVRDGNPY 60

QY 61 AYXDKCLKFSKISEYRHVCYSYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 GVCTCKLKFYSKISEFWYRSYVGETLEKLTNKKQLCDLLIRCTCQKPLCPBEKQRHLD 120  
QY 121 KQRFNIRGRWTRCSCCRSSRTRETQL 151  
DB 121 KKKRFNIGRWTRCSCCRSRTRETQV 149

## RESULT 4

W6WL33  
E6 protein - human papillomavirus type 33  
C/Species: human papillomavirus type 33  
C/Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004  
C/Accession: A03683  
R/Cole, S.T.; Strecek, R.E.  
J. Virol. 58; 991-995, 1986  
A/Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi  
A/Reference number: A93020; MUID:86200464; PMID:3009902  
A/Accession: A03683  
A/Molecule type: DNA  
A/Residues: 1-149 <COL>  
A/Cross-references: UNIPROT:P06427; UNIPARC:UPI00001383CD; GB:M12732; NID:G333049; PIDN:  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F/30-66/Region: zinc finger CCCC motif  
F/103-139/Region: zinc finger CCCC motif

Query Match 62.7%; Score 520; DB 1; Length 149;  
Best Local Similarity 63.6%; Pred. No. 1.9e-42;  
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTTHDILIECVYCKQQLLRREYDFAFADLCIYVRDGNPY 60  
DB 1 MFODTEKRPRLHDLCOALERTTHNIELOQVECKPLQSEYDFAFADLCIYVRREGNPF 60  
QY 61 AYXDKCLKFSKISEYRHVCYSYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRHLD 120  
DB 61 GICLCLKFLSKISEYHNYRSYVGNLTBQTVKKPLNEIIRICICQKPLCPBEKQRHVD 120  
QY 121 KQRFNIRGRWTRCSCCRSSRTRETQL 151  
DB 121 LNKRFNIGRWTRCSCCRSRTRETAL 149

## RESULT 5

W6WL58  
E6 protein - human papillomavirus type 58  
C/Species: human papillomavirus type 58  
A/Note: host Homo sapiens (man)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: E36779  
R/Kitil, Y.; Iwamoto, S.; Matsukura, T.  
Virology 185; 424-427, 1991  
A/Title: Human papillomavirus type 58 DNA sequence.  
A/Reference number: A36779; MUID:92024102; PMID:1656594  
A/Accession: E36779  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-149 <KIR>  
A/Cross-references: UNIPROT:P2655; UNIPARC:UPI000000081B; GB:D90400; NID:G222386; PIDN:  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F/30-66/Region: zinc finger CCCC motif  
F/103-139/Region: zinc finger CCCC motif

Query Match 59.8%; Score 496; DB 1; Length 149;  
Best Local Similarity 61.6%; Pred. No. 3.7e-40;  
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTTHDILIECVYCKQQLLRREYDFAFADLCIYVRDGNPY 60  
DB 1 MFODAEKRPRLHDLCOALERTSVHIELKCVCEKKTQLQSEYDFAFADLCIYVRDGNPF 60

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Qy      61 NVDDKCLKFYSKISRYRHCYCVGTTLEQQNKPFLCDLLIRINCXNQKPLCPERCKRHLD 120
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      61 AVCCVCTLRSLIKISEYRRHYNLSLYGDTEQLTKCLNEILIRCIICORPFCPOEKCHVD 120
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::

Oy      121 KGORFHNI RGRWTRGRCMCSCCRSTRRTRETOL 151
           :|||||:|||||: |||::|||::
Db      121 LNKRFPHNISGRWTGRCAVCWRP--RRROTQV 149

RESULT 6
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahnurachman, A.; Warza, U.
Int. J. Cancer 48, 516-522, 1991
A>Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma tissue
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Status: preliminary
A:Accession: A61237
A:Molecule type: DNA
A:Residues: 1-148 <TAK>
A:Cross-references: UNIPARC:UPI0000178415
A:Superfamily: papilliomavirus E6 protein
```

Query Match	58.7%	Score 487	DB 2	Length 148
Best Local Similarity	61.7%	Pred. No. 2.6e-39		
Matches	87	Conservative 19	Indels 0	Gaps 0
QY	1	MFODPOEPRKLPOLCTELQTTIHIIIECVYCKOOLLREAYVDAFRDLCTVARDGMPY	60	
Db	1	MFEDBATPRRLHETHELCEVLSEVHEIRLQCVQCKELQREREYKFLFDLRLVYDNNPY	60	
QY	61	AVXDCKLFEYSKISERYHYCYSVYGTLLBOQYNKELCDLLIRCIHXQKPLCEBKORHLD	120	
Db	61	GVCIMCJLRFSLKISIEYRHYQYSLVYKTLBERVRKSLTETIRCIICQPLPCEBKERYHN	120	
QY	121	KKORFHNIRGRWTCGMSCCR	141	
Db	121	ANKRPHNIMGRWTCGSECWR	141	

RESULT 7  
S36573 E6 protein - human papillomavirus type 52  
C:Species: human papillomavirus type 52  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36573  
R:Delius, H., Hofmann, B.  
A:Submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36573  
A:Molecule type: DNA  
A:Residues: 1-148 <DEL>  
A:Cross-references: UNIPROT:P36814; UNIPARC:UPI00001383DD; EMBL:X74481; NTD:g397038; PDB:1A98  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match	58.7%	Score 487	DB 2	Length 148
Beet Local Similarity	61.7%	Pred. No. 2.6e-39		
Matches 87	Conservative 19	Mismatches 35	Indels 0	Gaps 0
QY	1	MEODPQERPRRLPOLCTELQTTIHDIILECYCCQQLLRREYVDAPFDLCIVRDSNPY	60	
DB	1	MEEDPARRPRRLHETCEVLESVHEIRLQCVQCKKELORREYKFLFTDLRIIVYDDNNPY	60	
QY	61	AVXDKCLFYFKISIEYRHGYCVVGTTEEQYNNRPLGDLIRCIHXQKPLDPEEKGRILD	120	
DB	61	GVCLIMCLREFLSKISIEYRHGYQVSLGKLTLEENKPKLPSITTRCIIQPLPDPBEKERHVN	120	

```

QY      121 KKQRFHNRGRWTGRCMSCCR 141
      : ||||| ||||| |
DB      121 ANKRFHNRGRWTGRCSECCWR 141

```

RESULT 8  
S36515  
E6 protein - human papillomavirus type 34  
C:Species: human papillomavirus type 34  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36515

submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36515  
A:Molecule type: DNA  
A:Residues: 1-148 <DEL>  
A:Cross-References: UNIPROT:P36811, UNIPARC:UPI00001383CE, EMBL:X74476, NID:g336989, PID  
C:Superfamily: Papillomavirus E6 protein  
Keywords: DNA binding; early protein; nucleus; zinc finger

[illegible]

```

RESULT 9
M6WL51      B6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Jungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LIn>
A:Cross-references: UNIPROT:P26554; UNIPARC:UPI0000183DC; GB:M62877
C:Superfamily: papillomavirus B6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:/30-66/Region: zinc finger CCCC motif
F:/103-139/Region: zinc finger CCCC motif

```

	Query Match	55.4%	Score 460;	DB 1;	Length 151;
	Best Local Similarity	57.0%;	Pred. No. 1e-36;		
	Matches	86;	Conservative	24;	Mismatches 41; Indels 0; Gaps 0;
Qy	1 MFODPOBRPKLTCTELQTTHIDILCEYCGKQOLLRRVDFAFRDLCTIVRDGPNY	60			
	:   :   :   :   :   :   :   :   :				
Dd	1 MFEEDKRPRPTLHLCALNWSMHNIOVCYCKEELCRDADYNVAATEIIVTRDNPNY	60			
Qy	61 AVXDCLLFPSKISSEYRHVCYSVYGTLLEOQYNPLCDLLIRCNOKPLCPPEKORHL	120			
Dd	61 AVCKQCGLLFPSKIREYRYRSRVYGTLLLEATIKTSKYLDLSIRCHRCGRPLGPBEKQTV	120			
Qy	121 KQRFHNIRGRWTCRMSCCRSSRTRETQL	151			

Db 121 EKKRFHEIAGKWTGOCANCMQRTQRNETOV 151

## RESULT 10

S36561  
E6 protein - human papillomavirus type 45  
C:Species: human papillomavirus type 45  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
A:Accession: S36561  
R:Delius, H.; Hofmann, B.  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469

A:Molecule type: DNA  
A:Residues: 1-158 <DEL>  
A:Cross-references: UNIPROT:P21735; UNIPARC:UPI00001383D8; EMBL:X74479; NID:g397022; PID  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 55.4%; Score 459.5; DB 2; Length 158;  
Best Local Similarity 56.1%; Pred. No. 1.2e-36;  
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

Qy 2 FQDPQERPRKLPOLCTELQTTIHDIILECYVCKQQLRREYVDPAFRLCTIYRDGNPYA 61

Db 4 FDDPKQRPYKLPDLCETLNTSLQDVSIACVCKATLEKTEVYQFAFKDLCTIYRDCTAAYA 63

Qy 62 VXDCKLKFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCIINXQKPLCPCEKQRLDK 121

Db 64 ACHKCIPFYSIRIRLRNYSVSGTLEKINTLGNLYMLIRCLRCQKPLPAEKRLHND 123

Qy 122 KQRFNIRGRMTGRCMSCCRSS-----RTRETOL 151

Db 124 KRPFHNIAGYRGQCHSCCNRAQERLQRRETQV 158

## RESULT 11

W6WL18  
E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18  
C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
A:Accession: A26165; G26251  
R:Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.  
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16

A:Reference number: A91068; MUID:87218459; PMID:3034571  
A:Accession: A26165

A:Molecule type: DNA  
A:Residues: 1-158 <SRE>

A:Cross-references: UNIPROT:P06463; UNIPARC:UPI000002COFB; GB:X04773; NID:g60876; PIDN:C

R:Coile, S.T.; Danos, O.  
J. Mol. Biol. 193, 599-608, 1987

A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1

A:Reference number: A92937; MUID:87283882; PMID:3039146

A:Accession: G26251

A:Molecule type: DNA  
A:Residues: 1-158 <COL>

A:Cross-references: UNIPARC:UPI000002COFB; GB:X05015; NID:g60975; PIDN:CA28664.1; PID:G

R:MacLashewski, G.; Banks, L.; Wu-liao, J.; Spence, P.; Pim, D.; Crawford, L.  
J. Gen. Virol. 67, 1909-1916, 1986

A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p

A:Reference number: A92791; MUID:86306665; PMID:3018129  
A:Contents: annotation; identification of the protein  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:32-68/Region: zinc finger CCCC motif  
F:105-141/Region: zinc finger CCCC motif

Query Match 54.9%; Score 455.5; DB 1; Length 158;  
Best Local Similarity 56.1%; Pred. No. 2.8e-36;  
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Qy 2 FQDPQERPRKLPOLCTELQTTIHDIILECYVCKQQLRREYVDPAFRLCTIYRDGNPYA 61

Db 4 FEDPRRPRYKLPDLCETLNTSLQDIETTCVCKTVELTFEFAFKDLCTIYRDCTAAYA 63

Qy 62 VXDCKLKFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCIINXQKPLCPCEKQRLDK 121

Db 64 ACHKCIPFYSIRIRLRNYSVSGTLEKINTLGNLYMLIRCLRCQKPLPAEKRLHND 123

Qy 122 KQRFNIRGRMTGRCMSCCRSS-----RTRETOL 151

Db 124 KRPFHNIAGYRGQCHSCCNRAQERLQRRETQV 158

## RESULT 12

W6WL18  
E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180  
A:Note: host Homo sapiens (man)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

A:Accession: C40509  
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694

A:Accession: C40509

A:Molecule type: DNA  
A:Status: translation not shown

A:Residues: 1-158 <REU>

A:Cross-references: UNIPROT:P27962; UNIPARC:UPI00000082F; GB:M73258

C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:32-68/Region: zinc finger CCCC motif  
F:105-141/Region: zinc finger CCCC motif

Query Match 54.4%; Score 451.5; DB 1; Length 158;  
Best Local Similarity 55.1%; Pred. No. 6.8e-36;  
Matches 86; Conservative 21; Mismatches 44; Indels 5; Gaps 1;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYVCKQQLRREYVDPAFRLCTIYRDGNPY 60

Db 3 LFHNPBRPRYKLPDLCETLNTSLQDIETTCVCKTVELTFEFAFKDLCTIYRDCTAAYA 62

Qy 61 AYXDKLKFYSKISEYRHVCYVGTTLQOYNKPLCDLLIRCIINXQKPLCPCEKQRLDK 120

Db 63 AACOSCKFYAKIRLRNYSVSGTLEKINTLGNLYMLIRCLRCQKPLPAEKRLHND 122

Qy 121 KQRFNIRGRMTGRCMSCCRSS-----RTRETOL 151

Db 123 SKRPFHNIAGNFTGQCHCWTSKREDBRRRTRETQV 158

## RESULT 13

W6WL18  
E6 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39  
A:Note: host Homo sapiens (man)  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

A:Accession: A38502  
R:Volpers, C.; Strecek, R.E.

Virol. 181, 419-423, 1991

A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A:Reference number: A38502; MUID:9115017; PMID:1647266

A:Accession: A38502  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-158 <VOL>  
A:Cross-references: UNIPROT:P24835; UNIPARC:UPI00001383D2; GB:M62849; EMBL:M38185; NID:g

C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; transforming protein; zinc finger  
F:32-68/Region: zinc finger CCCC motif  
F:105-141/Region: zinc finger CCCC motif



```

Query Match      54.2%  Score 449.5: DB 1:  length 158;
Best Local Similarity 55.5%: Pred. 1.1e-35;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;

QY      2 FQDPERPRKLPOLCTELQTTIHDIILECVYCKQOQLRREYVDFAFRDLCTIVYRGNRYA 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4 FHNAERERYKLPDLCITLDTLQDITTIACVCRRLQGTVEFAFSDLVYVYVYRGEPLA 63
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      62 VXDCKLRKYSKISEVRHVCYVYGTTLEQOQNNKPLCDLLIRICINQKRLCPBEKORHLDK 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      64 ACQSCIKRYAKIRREIRYSDSVYATLTENITNTKYLLNLLIRMCCLKPLCPAEKRLRLNS 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      122 KQRFHNIIGRWTCRMCSCCRSSR-----TRRETOL 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      124 KRFHKLIAGSYTGCCRCRCMTTKREDRLTRRETQV 158
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

**RESULT 14**

E6 protein - rhesus papillomavirus (type 1)  
 C/Species: rhesus papillomavirus  
 C/Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C/Accession: A38503  
 R/Octrow, R.S.; Labresh, K.V.; Paras, A.J.  
 Virology 181, 424-429, 1991  
 A/Title: Characterization of the complete RhpV 1 genomic sequence and an integration loc  
 A/Reference number: A38503; PMID:91135018; PMID:1847267  
 A/Accession: A38503  
 A/Status: translation not shown  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-191 <OST>  
 A/Cross-references: UNIPROT:P22159; UNIPARC:UPI00001383BE; EMBL:M3717  
 C/Superfamily: papillomavirus E6 protein  
 C/Keywords: DNA binding; early protein; transforming protein; zinc finger  
 F:60-96/Region: zinc finger CCCC motif  
 F:133-169/Region: zinc finger CCCC motif

Query Match 52.8%; Score 438; DB 1; Length 191;

Best Local Similarity - 55.8%; Pred. No. 1.6e-34;  
Matches 82; Conservative 23; Mismatches 40; Indels 2; Gaps 1

Dy 4 DQERARKLPOLCTELOTTIHDIIECYCKOQLRREVYDFAFRDLCTVVRDGNPAVK 63  
Db 34 EPNELPRTIHEICEGRETTLHLEQLCYVCLKELTRIEVYDFARMDLRVLVHRGKPYGVC 93

Dy 64 DKCLKFSKTSSEYRHYCYSTVGTTEEQYNPKLDDLIRCTINXQKPRLCEEKHRLDKQ 123  
||:||||:|:||:||||:::||||| ||||| ||||| :|  
Db 94 PICLRFSKTRKYRYEYSTIGCTLEARTRKQLVEVLIRCYCCQKPLPIEKRRHVDGQ 153

```

QY. 124 RFHNRGRWTRGRCMSCCRSSRTTRRETQ 150
      ||| : |||| : |||
Db   154 RFHRIAGQWTRGRLMCWRP--TVPETQ 178

```

### RESULT 15

E6 protein - human papillomavirus type 26

C:Species: human papillomavirus type 26

```
C:\Acceesion: S36544
C:\Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
```

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-dire

A;reference number: S36544

A: Molecule type: DN  
 A: Accession: 050544

A;Residues: 1-150 &lt;DEL&gt;

A; Cross-references: UNIPROT:P36807; UNIPARC:UPI00001383C5; EMBL:X74472; NID:g396956; PIR:

C;Superfamily: papillomavirus E6 protein

**Keywords:** early protein; zinc finger

Query Match	52.6%	Score 436.5	DB 2	Length 150
-------------	-------	-------------	------	------------

Best Local Similarity 55.0%; Pred. No. 1.7e-34;

Matches 83; Conservative 24; Mismatches 43; Indels 1; Gaps 1;

Qy 1 MPDQPERPRKJ.POLCTELQTTIHIIIECYCKQOLLRREYDQFARFDICIVARDNPY 60  
 Qy 1 MEEDPRPERPRRTJHELCESINTLTQNIQVOCYCKKETLOMADVNPALCDLREVVRRDSRY 60  
 Qy 1 AYVADCKLKEYSKISEYRHYCVYGTLEEOQNNPKDCLLRICINXQKPLCPPEKORHL 120  
 Db 61 ACKRCVIFYSKITEYRRTYSCVSGATIEALTKKSLCNLLRRCQMPLEPEKQIVD 120  
 Qy 121 KKRHHNRGRTGRCMCCSSRRRRRTOL 151  
 Db 121 EKRRFHEIAGQMKGLCTQNCMR-PRQCTEQV 150

Search completed: June 6, 2006, 12:11:55  
Job time : 30.1084 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

# OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:34 ; Search time 232.867 Seconds  
(without alignments)  
599.815 Million cell updates/sec

Title: US-10-530-253-13  
Perfect score: 830  
Sequence: 1 MFQDPQRRPRRLPOLCTELQ.....WTGRCMSCCRSSRRRTETQL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	151	2	077JCT_HPV16
2	826	99.5	151	2	089852_9PAP1
3	826	99.5	158	2	09WH13_HPV16
4	824	99.3	151	2	09WMP3_HPV16
5	823	99.2	151	2	077816_HPV16
6	823	99.2	151	2	089755_9PAP1
7	823	99.2	151	2	08BB20_HPV16
8	823	99.2	158	1	VE6_HPV16
9	823	99.2	158	2	054702_HPV16
10	823	99.2	161	2	0919C6_HPV16
11	821	98.9	151	2	08BB19_HPV16
12	821	98.9	158	2	04VRN5_HPV16
13	820	98.8	158	2	08ORD7_HPV16
14	820	98.8	158	2	08ORD8_HPV16
15	819	98.7	151	2	0772J5_HPV16
16	819	98.7	151	2	089640_9PAP1
17	819	98.7	151	2	089648_9PAP1
18	819	98.7	151	2	09W931_HPV16
19	819	98.7	158	2	02PJN9_HPV16
20	819	98.7	158	2	08OHT0_HPV16
21	818	98.6	151	2	080963_9PAP1
22	818	98.6	158	2	08OHP5_HPV16
23	817	98.4	151	2	08B564_9PAP1
24	817	98.4	151	2	09W8C3_HPV16
25	817	98.4	151	2	0919D4_HPV16
26	816	98.3	158	2	08ORD9_HPV16
27	816	98.3	158	2	08ORD0_HPV16
28	816	98.3	158	2	09QDH9_HPV16
29	815	98.2	151	2	089887_9PAP1
30	815	98.2	158	2	08ORD5_HPV16
31	814	98.1	158	2	08ORD6_HPV16

32	814	98.1	158	2	09QDH3_HPV16	09qdh3 human papil
33	814	98.1	161	2	0919B1_HPV16	0919b1 human papil
34	813	98.0	158	2	08QRE1_HPV16	08qre1 human papil
35	812	97.8	151	2	012335_HPV16	012335 human papil
36	811	97.7	151	2	09WMP4_HPV16	09wmp4 human papil
37	810	97.6	151	2	012336_HPV16	012336 human papil
38	809	97.5	158	2	09QDH7_HPV16	09qdh7 human papil
39	808	97.3	151	2	08BB21_HPV16	08bb21 human papil
40	808	97.3	151	2	09WMP2_HPV16	09wmp2 human papil
41	808	97.3	161	2	0919A9_HPV16	0919a9 human papil
42	806	97.1	151	2	076TS0_9PAP1	076ts0 human papil
43	806	97.1	151	2	080966_HPV16	080966 human papil
44	806	97.1	158	2	08JMU8_HPV16	08jmu8 human papil
45	804	96.9	151	2	077E16_HPV16	077e16 human papil

## ALIGNMENTS

RESULT 1  
077JCT\_HPV16  
ID 077JCT\_HPV16 PRELIMINARY; PRT; 151 AA.  
AC 077JCT;  
DT 05-JUN-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUN-2004, sequence version 1.  
DT 07-FEB-2006, entry version 12.  
DE Early transforming protein E6 variant (Transforming protein E6).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Xinjiang.  
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang O., Zhang F.;  
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma  
RT Biopsies in Xinjiang."  
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;  
RA Derflinger V.R., Ayala F.U., Villareal L.P.;  
RT "Evidence of diversifying selection in human papillomavirus type 16 E6  
RT but not E7 oncogenes.";  
RL J. Mol. Evol. 55:491-499(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.F.;  
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RA Cruz M.R., Martins C.R.F.;  
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL; AF37851; AAG5940.1; -; Genomic DNA.  
CC EMBL; AJ388057; CAB45106.1; -; Genomic DNA.  
CC EMBL; AJ388059; CAB4510.1; -; Genomic DNA.  
CC EMBL; AY089951; AAM11875.1; -; Genomic DNA.  
CC EMBL; AY089954; AAM11881.1; -; Genomic DNA.  
CC EMBL; AY112663; AAM51854.1; -; Genomic DNA.  
CC GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 99.5%; Score 826; DB 2; Length 151;
Best Local Similarity 98.7%; Pred. No. 2.4e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 60
QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
DB 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
DB 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151

RESULT 2
Q89852_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q89852_9PAPI
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments."
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: U34134; AAA91681.1; -; Genomic DNA.
DR EMBL: U34127; AAA91674.1; -; Genomic DNA.
DR EMBL: U34133; AAA91680.1; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 99.5%; Score 826; DB 2; Length 151;
Best Local Similarity 98.7%; Pred. No. 2.4e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 60
QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
DB 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
DB 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
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DB 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151

RESULT 3
Q9WH13_HPV16 PRELIMINARY; PRT; 158 AA.
ID Q9WH13_HPV16
AC Q9WH13_
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 19.
DE E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9668;
RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;
RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle
RT in an immortalized human foreskin keratinocyte cell line."
RL J. Virol. 262:344-354(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-C109G;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1006/342048;
RA Chan P.K.S., Lam C.W., Chung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China."
RL J. Infect. Dis. 186:696-700(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV16936E;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RT on complete genome analyses."
RL J. Virol. 79:7014-7023(2005).
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CC -----
DR EMBL: AF125673; AAD33252.1; -; Genomic DNA.
DR EMBL: AF466322; AAY96627.1; -; Genomic DNA.
DR EMBL: AY686580; AAY91652.1; -; Genomic DNA.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19173 MW; 9F0CF5ADDA2ED7FE CRC64;

Query Match 99.5%; Score 826; DB 2; Length 158;
Best Local Similarity 98.7%; Pred. No. 2.5e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVYDFAFRDLCTIVRDGNY 67
QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 120
DB 68 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLIRCNXOKPLCPBEKQRLD 127
QY 121 KKQRFHNIRGRWTRCSCSSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRCSCSSSRTRETOL 158

RESULT 4
Q9WMP5_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9WMP5_HPV16
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AC O9WMP5;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN
RP NUCLEOTIDE SEQUENCE.
RA Duin M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; AJ242681; CAB45381.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2D5FD93F8917 CRC64;

Query Match 99.3%; Score 824; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 3.8e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
QY 61 AVXDKLKFYSKISRYHYCVSVGTTLQOYNKPLCDLLIRCIKXQKPLCEEKQRHLD 120
DB 61 AVXDKLKFYSKISRYHYCVSVGTTLQOYNKPLCDLLIRCIKXQKPLCEEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRRRTTOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRRRTTOL 151

RESULT 5
Q77816_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q77816_HPV16
AC Q77816;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; Pubmed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN
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DR EMBL; AJ388056; CAB45104.1; -; Genomic DNA.
DR EMBL; AJ388061; CAB45114.1; -; Genomic DNA.
DR EMBL; AJ388066; CAB45124.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F8F2A2FCEBA6C02 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
QY 61 AVXDKLKFYSKISRYHYCVSVGTTLQOYNKPLCDLLIRCIKXQKPLCEEKQRHLD 120
DB 61 AVXDKLKFYSKISRYHYCVSVGTTLQOYNKPLCDLLIRCIKXQKPLCEEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRRRTTOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRRRTTOL 151

RESULT 6
Q89755_9PAPI PRELIMINARY; PRT; 151 AA.
ID Q89755_9PAPI
AC Q89755;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Unclassified Papillomaviridae.
OX NCBI_TaxID=10566;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; Pubmed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jensen S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN
RP NUCLEOTIDE SEQUENCE.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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CC
EMBL; U34126; AA91673.1; -; Genomic DNA.
EMBL; U34111; AA91658.1; -; Genomic DNA.
DR EMBL; U34121; AA91668.1; -; Genomic DNA.
DR EMBL; U34123; AA91670.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F8F2A2FCEBA6C02 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGNPY 60
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Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Qy 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 7
Q8BB20 HPV16 PRELIMINARY; PRT; 151 AA.
ID Q8BB20 HPV16 PRELIMINARY; PRT; 151 AA.
AC Q8BB20
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Deillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
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CC -----
DR EMBL: AY089953; AAM1879.1; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 7CBD23EFCF4F8C17 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Db 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Qy 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 121 KKQRFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 8
VE6_HPV16 STANDARD; PRT; 158 AA.
ID VE6_HPV16 STANDARD; PRT; 158 AA.
AC P03126; Q71B17;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Protein E6.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Dürst M., Suhai S., Rowekamp W.G.;
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```
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Isolate European German 131;
RA Terai M., Fu L., Ma Z., Burk R.D.;
RT "Cloning and sequencing of non-European human papillomavirus (HPV)
variant complete genomes from cervicovaginal cells by an overlapping
PCR method."
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 31-50.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Behau-Arnaudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia."
RL J. Gen. Virol. 71:809-817(1990).
RN [4]
RP INTERACTION WITH HUMAN FBIN1, AND INHIBITION OF E6-MEDIATED
RP TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.U.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1."
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
CC protein ligase, the human TP53/p53 tumor suppressor protein by
CC targeting it to degradation. Binds and targets human MDM1/MDM2
CC protein to degradation. Those two functions presumably contribute
CC to transforming activity (By similarity). Interaction with human
CC FBIN1 protein also seems to be linked to cell transformation.
CC -1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which
CC interacts with human p53. Binds to human FBIN1 and MDM2 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -1- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
CC -----
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CC -----
DR EMBL: K02718; AAA46939.1; Genomic DNA.
DR EMBL: AF536179; AA010712.1; Genomic DNA.
DR EMBL: D00735; BA00632.1; Genomic DNA.
DR PIR: A03682; W6WHS.
DR PDB: 2FK4; NMR; A=87-158.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR 3D-structure: Activator; DNA-binding; Early protein; Metal-binding;
KW Nuclear protein; Oncogene; Transcription; Transcription regulation;
KW Zinc; Zinc-finger.
FT CHAIN 1 158
FT FT
FT ZN_FING 37 73
FT ZN_FING 110 146
FT MOTIF 155 158
FT MOTIF 17 17
FT CONFLICT 90 90 R -> G (in Ref. 2).
FT CONFLICT 90 90 L -> V (in Ref. 2).
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCFB37EB CRC64;

Query Match 99.2%; Score 823; DB 1; Length 158;
Best Local Similarity 98.0%; Pred. No. 4.9e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Db 8 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 67
Qy 61 AVXDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVCYSVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 127
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Qy 121 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 151  
Db 128 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 158

RESULT 9  
ID 054732 HPV16 PRELIMINARY; PRT: 158 AA.  
AC 054732 HPV16  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Transforming protein E6.  
GN Name:E6;  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN:E-6, E-G187T, and E-G538T;  
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;  
RT "Human papillomavirus type 16 intratypic variant infection and risk  
RT for cervical neoplasia in southern China.";  
RL J. Infect. Dis. 186:696-700(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN:Qv17722E, and Qv15521E;  
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;  
RA Chen Z., Terai M., Fu L., Herrero R., Desai R., Burk R.D.;  
RT "Diversifying selection in human papillomavirus type 16 lineages based  
RT on complete genome analyses.";  
RL J. Virol. 79:7014-7023(2005).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN:Beb-102;  
RA Cruz M.R., Cerveira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,  
RA Martins C.R.P.;  
RT "Human papillomavirus type 16 variants in Central Brazil.";  
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.  
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CC  
CC EMBL: AF486311; AAL96616.1; -; Genomic DNA.  
DR EMBL: AY686584; AAV91684.1; -; Genomic DNA.  
DR EMBL: AF486310; AAL96615.1; -; Genomic DNA.  
DR EMBL: AF486312; AAL96617.1; -; Genomic DNA.  
DR EMBL: AF486313; AAL96618.1; -; Genomic DNA.  
DR EMBL: AF486317; AAL96622.1; -; Genomic DNA.  
DR EMBL: AF486320; AAL96625.1; -; Genomic DNA.  
DR EMBL: AF486321; AAL96626.1; -; Genomic DNA.  
DR EMBL: AY098919; AAM29167.1; -; Genomic DNA.  
DR EMBL: AY686581; AAM29166.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFB37EB CRC64;

Query Match 99.2%; Score 823; DB 2; Length 158;  
Best Local Similarity 98.0%; Pred. No. 4.9e-73;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 60  
Db 8 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 67

Qy 61 AVXKCLKFKYSKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 120  
Db 68 AVXKCLKFKYSKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 127

Qy 121 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 151

Db 128 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 158

RESULT 10  
ID 0919C6 HPV16 PRELIMINARY; PRT: 161 AA.  
AC 0919C6 HPV16  
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;  
RA Watts K.J., Thompson C.H., Cozzare Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
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CC  
CC EMBL: AF404697; AAL01351.1; -; Genomic DNA.  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1  
SQ SEQUENCE 161 AA; 19628 MW; 15D32F0F12E00460 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 161;  
Best Local Similarity 98.0%; Pred. No. 5e-73;  
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 60  
Db 11 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 70

Qy 61 AVXKCLKFKYSKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 120  
Db 71 AVXKCLKFKYSKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 130

Qy 121 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 151  
Db 131 KKORFHNIRGWTGRCSGCCSSRTTRRETOL 161

RESULT 11  
ID 08B319 HPV16 PRELIMINARY; PRT: 151 AA.  
AC 08B319 HPV16  
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
DT 01-MAR-2003, sequence version 1.  
DT 07-FEB-2006, entry version 13.  
DE Early transforming protein E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22424222; PubMed=12356268; DOI=10.1007/s00239-002-2344-Y;  
RA DePillipe V.R., Ayala F.J., Villarreal L.F.;  
RT "Evidence of diversifying selection in human papillomavirus type 16 E6  
RT but not E7 oncogenes.";  
RL J. Mol. Evol. 55:491-499(2002).  
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DR EMBL; AY089955; AAM1883.1 -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18319 MW; 6F9D2A2FDSA8F8F7 CRC64;

Query Match          98.9%; Score 821; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 7.4e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCCKQQLRREYVDFARFDCIYVRDGNPY 60
DB 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCCKQQLRREYVDFARFDCIYVRDGNPY 60
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 120
DB 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 120
QY 68 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 127
DB 68 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 127
QY 121 KKQRFHNIRGRWTCGSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTCGSCSSSRTRETOL 151
QY 128 KKQRFHNIRGRWTCGSCSSSRTRETOL 158
DB 128 KKQRFHNIRGRWTCGSCSSSRTRETOL 158

RESULT 12
Q4VRN5_HPV16 PRELIMINARY; PRT; 158 AA.
ID Q4VRN5;
AC Q4VRN5;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=QV18158E;
RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terzi M., Fu L., Herrero R., Desalle R., Buck R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RT on complete genome analyses.";
RL J. Virol. 79:7014-7023(2005).
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-----
DR EMBL; AY686583; AAV91676.1 -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 158 AA; 19172 MW; 91ECF5ADD4CED31E CRC64;

Query Match          98.9%; Score 821; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 7.8e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCCKQQLRREYVDFARFDCIYVRDGNPY 60
DB 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCCKQQLRREYVDFARFDCIYVRDGNPY 67
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 120
DB 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 120
QY 68 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 127
DB 68 AVCDKCLKFYSKISEYRHVCYSVYGTLEQQYNKPLCDLLIRCIKXQKPLCPCEKQKHLD 127
QY 121 KKQRFHNIRGRWTCGSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTCGSCSSSRTRETOL 151
QY 128 KKQRFHNIRGRWTCGSCSSSRTRETOL 158
DB 128 KKQRFHNIRGRWTCGSCSSSRTRETOL 158

RESULT 13
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OQQRD7_HPV16 PRELIMINARY; PRT; 158 AA.
ID OQQRD7_HPV16
AC OQQRD7;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-C442T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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-----
OQQRD8_HPV16 PRELIMINARY; PRT; 158 AA.
ID OQQRD8_HPV16
AC OQQRD8;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=E-G449T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
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DR EMBL: AF486316; AAL96621.1; -: Genomic DNA.  
DR GO: 0042025; C:host cell nucleus; IEA.  
DR GO: 0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 158 AA; 19188 MW; 01FEF5B1D21AF7EB CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;  
Best Local Similarity 97.4%; Pred. No. 9.8e-73;  
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60  
DB 8 MFODPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 67  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 68 AVXDCKLKFYSKISRYHYCYSVYGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127  
QY 121 KKORFHNIRGRWTCRSCSSRTRETOL 151  
DB 128 KKORFHNIRGRWTCRSCSSRTRETOL 158

## RESULT 15

077ZJ5 HPV16 PRELIMINARY; PRT; 151 AA.  
ID 077ZJ5;  
AC 077ZJ5;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE E6 protein.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=97437474; PubMed=9292007;  
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,  
RA Beth-Giraldo E., Giraldo G.;  
RT "Sequence variations and viral genomic state of human papillomavirus  
RT type 16 in penile carcinomas from Ugandan patients.";  
RT J. Gen. Virol. 78:2199-2208 (1997).  
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CC -----  
DR EMBL: AF003019; AAB70736.1; -: Genomic DNA.  
DR EMBL: AF003018; AAB70735.1; -: Genomic DNA.  
DR GO: 0042025; C:host cell nucleus; IEA.  
DR GO: 0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 151 AA; 18221 MW; 60CDD2A34DAF48CB7 CRC64;

Query Match 98.7%; Score 819; DB 2; Length 151;  
Best Local Similarity 98.0%; Pred. No. 1.2e-72;  
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60  
DB 1 MFODPQERPRKLPQCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60  
QY 61 AVXDCKLKFYSKISRYHYCYSVYGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
DB 61 AVXDCKLKFYSKISRYHYCYSVYGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120  
QY 121 KKORFHNIRGRWTCRSCSSRTRETOL 151  
DB 121 KKORFHNIRGRWTCRSCSSRTRETOL 151

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Wed Jun 7 12:17:52 2006

us-10-530-253-14.rag

Page 1

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:15 ; Search time 143.655 Seconds  
(without alignments)  
311.909 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517

Sequence: 1 MHGDTPTLHEFMLDQPEPTT.....LEDLLMGTGLGVPCSGKP 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*
- 10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	8	AD044070
2	513	99.2	98	8	AED13079
3	513	99.2	220	2	AAV25378
4	513	99.2	220	2	AAV02634
5	513	99.2	220	9	AED52640
6	513	99.2	248	8	AD044068
7	513	99.2	805	6	ADA27366
8	513	99.2	805	7	ADA92544
9	513	99.2	805	7	ADA14293
10	513	99.2	805	7	AAE38618
11	512	99.0	98	2	AAE22767
12	512	99.0	98	2	AAE42361
13	512	99.0	98	2	AAW46886
14	512	99.0	98	3	AAV58474
15	512	99.0	98	3	AAV57721
16	512	99.0	98	4	AAV98421
17	512	99.0	98	4	AAU01718
18	512	99.0	98	4	AAU72607
19	512	99.0	98	4	AAE67546
20	512	99.0	98	4	AAE86332
21	512	99.0	98	5	AAU77713
22	512	99.0	98	5	AAU10810
23	512	99.0	98	5	ABB82375

24	512	99.0	98	6	AAO16630	AAO16630 Human pap
25	512	99.0	98	7	ADP09516	ADP09516 Human pap
26	512	99.0	98	7	ADP18632	ADP18632 Human pap
27	512	99.0	98	8	ADL90076	ADL90076 Human pap
28	512	99.0	98	8	ADM32916	ADM32916 Human pap
29	512	99.0	98	8	AD044073	AD044073 Amino aci
30	512	99.0	98	8	ADN49005	ADN49005 Human pap
31	512	99.0	98	8	ADU66362	ADU66362 Human pap
32	512	99.0	98	9	ADX15532	ADX15532 Human pap
33	512	99.0	98	9	ADY69083	ADY69083 HPV_16 E7
34	512	99.0	98	9	AEA40816	AEA40816 Anti-apop
35	512	99.0	98	9	AEH11989	AEH11989 HPV16 E7
36	512	99.0	98	9	AEC96392	AEC96392 HPV prote
37	512	99.0	98	9	AEC98871	AEC98871 HPV_16 En
38	512	99.0	98	9	AED13078	AED13078 HPV16 E7
39	512	99.0	98	9	AED64360	AED64360 Human pap
40	512	99.0	98	10	AEE94089	AEE94089 HPV16 E7
41	512	99.0	99	8	AD088451	AD088451 HPV16 E7
42	512	99.0	99	9	ADY92615	ADY92615 HPV16 E7
43	512	99.0	121	4	AAE31608	AAE31608 Amino aci
44	512	99.0	198	4	AAE31616	AAE31616 Amino aci
45	512	99.0	212	8	ADT75831	ADT75831 Novel Fve

## ALIGNMENTS

RESULT 1	AD044070	standard; protein; 248 AA.
ID	AD044070	
XX	AD044070;	
DT	15-JUL-2004	(first entry)
XX		
DE	Amino acid sequence of a fusion protein designated E7B6Pentm.	
XX		
KM	B6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;	
KW	cervical cancer; immune response; lower gastrointestinal tract cancer;	
KM	anal cancer; reproductive system cancer; penile cancer; vulvar cancer;	
KW	gene; ss.	
OS	Human papillomavirus type 16.	
OS	Synthetic.	
XX		
PN	WO2004030636-A2.	
XX		
PD	15-APR-2004.	
XX		
PF	02-OCT-2003; 2003WO-US031726.	
XX		
PR	03-OCT-2002; 2002US-0415929P.	
XX		
PA	(AMHP ) WYETH HOLDINGS CORP.	
XX		
PI	Smith L, Casasetti MC;	
XX		
DR	WPI; 2004-316328/29.	
XX		
XX	N-PSDB; AD044071.	
PT	New polypeptide comprising human papillomavirus E6 and E7 polypeptides;	
PT	useful for treating or preventing human papillomavirus (HPV)-associated	
XX	cancers, e.g. cervical cancer.	
XX		
PS	Claim 22; Page 75-76; 101pp; English.	
XX		
CC	The present sequence represents a fusion protein, comprising E7 and E6	
CC	polypeptides from human papillomavirus type 16 (HPV16). The fusion	
CC	protein is designated E7B6Pentm, and comprises an E7 amino terminus	
CC	(where residues 24, 26 and 91 have been replaced with glycine) and an E6	
CC	carboxy terminus (where residues 63 and 106 have been replaced with an	
CC	glycine). E7B6Pentm is representative of fusion proteins of the	
CC	invention. The specification describes human papillomavirus E6 and E7	

polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of the sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.

**SQ Sequence 248 AA;**

Query Match	99.4%	Score 514	DB 8	Length 248
Best Local Similarity	96.9%	Pred. No. 3.9e-57		
Matches 95	Conservative	0	Mismatches 3	Indels 0
				Gaps 0

```
Qy      1 MHGDTPTLHEHYMDLOPETTTDLXXYYXQLNDSSEEDIDGPAGQAAPDRAHYNIWTFCKK 60
        |||||
Db      1 MHGDTPTLHEHYMDLOPETTTDLYGYGLNDSSEEDIDGPAGQAAPDRAHYNIWTFCKK 60
```

[illegible]

RESULT 2  
AED13079  
ID AED13079 standard; protein; 98 AA.

DT 15-DEC-2005 (first entry)

DE	HPV16 E7 variant protein sequence.
XX	
KW	mutagen; vaccine; antigen; virucide; antibacterial.

OS	Human papillomavirus type 16.
XX	
PN	FR2868781-A1.

PD	14-OCT-2005.
XX	
PF	13-APR-2004; 2004FR-00003848.

13-APR-2004; 2004FR-00003848.  
XX  
PA (IMMU-) IMMUTEP.

PI Triebel F;  
XX  
DR WPI; 2005-678227/70.

PT Therapeutic vaccine, for viral and bacterial conditions, comprises an  
PT antigen protein and a viral or bacterial protein, coupled together by

PS Disclosure; Fig 1; 51pp; French.

CC The invention relates to a novel vaccine composed of an antigen protein  
CC and a second protein as an S-(methyl mercury)-1-cysteine (CMH class II)  
CC

CC Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or  
CC bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures  
CC

CC (HIV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-  
CC Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The

CC and listeria. A vaccine of the invention has virucide, and antibacterial activity. The present sequence represents the HPV16 variant E7 protein

CC	sequence.
XX	
SQ	Sequence

**SQ** Sequence 98 AA;

Query Match	99.2%	Score 513	DB 9	Length 98
Best Local Similarity	96.9%	Pred. No. 1.6e-57		
Matches 95	Conservative 0	Mismatches 3	Indels 0	Gaps 0

Qy 1 MHGDPPTLHEXMLDLPETTTDLYXXXLNDSSSEEDLIDGPAGAEPPDRAHYNIVTFCK 600

Db 1 MHGDPPTLHEXMLDLPETTTDLYGYGLNDSSSEEDLIDGPAGAEPPDRAHYNIVTFCK 600

<b>Qy</b>	61 CSTLRICVGSHTVDIRLTLEDLLMGLTGIYAPICSKP 98
<b>Dd</b>	61 CSTLRICVGSHTVDIRLTLEDLLMGLTGIYAPICSKP 98

RESULT 3  
AAV25378  
ID AAV25378 standard; protein; 220 AA

AC	AAV25378;
XX	
DT	06-SEP-1999 (first entry)

DE HPV fusion protein D1/3-E7-Mutated(C24G, E26Q)/HPV16

KW Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour  
KW immunological fusion partner; CPG oligonucleotide; immune response;  
KW HPV antigen; prevention; treatment.

OS	Synthetic.
OS	Human papillomavirus.
XX	

XX 08-JUL-1999.  
PD  
XX

XX	24-DEC-1997;	97GB-00027262.
PR		
XX		

XX Dalemans WLU, Gerard CMG;  
XX  
XX

DR	N-PSDB; AAX78794.
XX	
PT	Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to

XX Example V; Page 51; 62pp; English  
PS  
XX

CC AA378792.478801 represent nucleic acid sequences which encode novel  
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
CC HPV (represented in AA355375-125386). These constructs are optionally  
CC linked to an immunological fusion partner and an immunomodulatory C66  
CC oligonucleotide. The products of the invention can be used to induce an  
CC immune response in a patient to an HPV antigen. They can also be used for  
CC preventing or treating HPV induced tumours

**SQ** Sequence 220 AA;

Query Match	99.2%	Score 513	DB 2	Length 220
Best Local	96.9%	Pred. NC	4.6e-57	
Matches 95	Conservative 0	Mismatches 3	Indels 0	Gaps 0

1 MHGDPTLHEWLDLPETTDLYXXKQUNDSSEDELDGPAGAAEPDRAHNYITPCCK 60

QY 61 CDSTRLCVOSTHVDIRTELEDLLMGLGIYXPICSQKP 98

Db 174 CDSTLRUCVOSTHVDIRLTEDLMGTGIVCPICSKP 211

|||||

RESULT 4  
AA02634  
ID AA02634 standard; protein; 220 AA.  
XX  
AC AA02634;  
XX  
DT 17-OCT-2003 (revised)  
DT 22-JUN-1999 (first entry)  
XX  
DE Prot.D1/3-E7-mut(C24G,E26Q)/HPV16 protein.  
XX  
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
KW tumour; lesion; benign; malignant; virus; infection.  
XX  
OS Human papillomavirus.  
OS Haemophilus influenzae.  
OS Chimeric.  
XX  
PN WO9910375-A2.  
XX  
PD 04-MAR-1999.  
XX  
PF 17-AUG-1998; 98WO-EP005285.  
XX  
PR 22-AUG-1997; 97GB-00017953.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
PI Lombardo-Bencheikh A;  
XX  
DR WPI: 1999-190587/16.  
DR N-PSDB: AAX29783.  
XX  
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
PT treatment or prophylaxis of HPV induced lesions.  
XX  
PS Disclosure; Fig 8; 95pp; English.  
XX  
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
CC partner, in this case, a fragment of the Haemophilus influenzae B protein  
CC D. The sequence also contains a histidine tag at the C-terminus of the  
CC encoded protein. The protein can be used in a vaccine, for immuno-  
CC therapeutically treating HPV induced tumour lesions (benign or malignant)  
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 220 AA;

Query Match 99.2%; Score 513; DB 2; Length 220;  
Best Local Similarity 96.9%; Pred. No. 4.6e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIVTFCK 60  
Db 114 MHGDPPTLHEHMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIVTFCK 173

QY 61 CDSTLRUCVOSTHVDIRLTEDLMGTGIVCPICSKP 98  
Db 174 CDSTLRUCVOSTHVDIRLTEDLMGTGIVCPICSKP 211

RESULT 5  
AED52640  
ID AED52640 standard; protein; 220 AA.  
XX  
AC AED52640;  
XX

DT 29-DEC-2005 (first entry)  
XX  
DE Fusion protein D1/3-E7-His(HPV16), C137G/E139Q.  
XX  
KW Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;  
KW virucide; uterine cervix tumor; E7; mucin; D protein.  
XX  
OS Haemophilus influenzae; strain 772.  
OS Human papillomavirus type 16.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 137  
FT /note= "Wild-type Cys substituted by Gly"  
FT Misc-difference 139  
FT /note= "Wild-type Glu substituted by Gln"  
XX  
PN IN9801903-14.  
XX  
PD 04-MAR-2005.  
XX  
PF 24-AUG-1998; 98IN-CH001903.  
XX  
PR 22-AUG-1997; 97EP-00179535.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Tyrrell AMR;  
XX  
DR WPI: 2005-557648/57.  
DR N-PSDB: AED52639.  
XX  
PT Vaccine.  
XX  
PS Example 8; Fig 8; 96pp; English.  
XX  
CC The invention relates to human Papilloma virus (HPV) fusion proteins,  
CC linked to an immunological fusion partner that provides T helper epitopes  
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins  
CC are useful in the treatment or prophylaxis of HPV induced lesions  
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7  
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either  
CC Haemophilus influenzae D protein (20-127), the C-terminus of  
CC Streptococcus pneumoniae LytA protein (cLYtA) or thiorodoxin. The present  
CC sequence represents a mutated HPV-H. influenzae D protein, fusion protein  
CC of the invention.  
XX  
SQ Sequence 220 AA;

Query Match 99.2%; Score 513; DB 9; Length 220;  
Best Local Similarity 96.9%; Pred. No. 4.6e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIVTFCK 60  
Db 114 MHGDPPTLHEHMDLQPEETDLYXXQLNDSSEEDIDGPAQAEPRRAHYNIVTFCK 173

QY 61 CDSTLRUCVOSTHVDIRLTEDLMGTGIVCPICSKP 98  
Db 174 CDSTLRUCVOSTHVDIRLTEDLMGTGIVCPICSKP 211

RESULT 6  
ADO44068  
ID ADO44068 standard; protein; 248 AA.  
XX  
AC ADO44068;  
XX  
DT 15-JUN-2004 (first entry)  
XX  
DE Amino acid sequence of a fusion protein designated E7E6retw.  
XX

KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
KM cervical cancer; immune response; lower gastrointestinal tract cancer;  
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
XX  
OS Human papillomavirus type 16.  
OS Synthetic.  
XX  
PN WO2004030636-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 02-OCT-2003; 2003WO-US031726.  
XX  
PR 03-OCT-2002; 2002US-0415929P.  
XX  
PA (AMHP ) WYETH HOLDINGS CORP.  
XX  
PI Smith L, Caesetti MC;  
XX  
DR WPI: 2004-316328/29.  
XX  
DR N-PSDB; ADA04069.  
XX  
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
PT useful for treating or preventing human papillomavirus (HPV)-associated  
PT cancers, e.g. cervical cancer.  
XX  
PS Claim 22; Page 73-74; 101pp; English.  
XX  
XX The present sequence represents a fusion protein, comprising E7 and E6  
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion  
CC protein is designated E7E6terw, and comprises an E7 amino terminus (where  
CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy  
CC terminus (where residues 63 and 106 have been replaced with glycine).  
CC E7E6terw is representative of fusion proteins of the invention. The  
CC specification describes human papillomavirus E6 and E7 polypeptides,  
CC where the E7 polypeptide has mutations at any one or more of the amino  
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
CC the sequence given in ADO44072. The polypeptides of the invention are  
CC useful for treating or preventing human papillomavirus (HPV)-associated  
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
CC encoding the fusion proteins are useful for generating immune responses  
CC against HPV. They are also useful for treating lower gastrointestinal  
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
CC system, including penile and vulvar cancer.  
XX  
SQ Sequence 248 AA:  
Query Match 99.2%; Score 513; DB 8; Length 248;  
Best Local Similarity 96.9%; Pred. No. 5.3e-57; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;  
QY 1 MHGDTPTLHEHYMDLOPETTDLYXXYXQINDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60  
Db 1 MHGDTPTLHEHYMDLOPETTDLYGYGQINDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60  
QY 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98  
Db 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98  
Db 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98  
RESULT 7  
ADA27366  
ID ADA27366 standard; protein; 805 AA.  
XX  
AC ADA27366;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.  
XX  
KM cell line; American Type Culture Collection PTA-4047; ATCC-4047;

KM baculoviruses; viral recombinant protein; virus-like particle; vaccine;  
KM diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/E2;  
KM fusion protein.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
PN WO2003068804-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004516.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
XX (NOVA-) NOVAVAX INC.  
XX  
PA Robinson RA;  
XX  
PI WPI: 2003-646475/61.  
XX  
DR WPI: 2003-646475/61.  
XX  
DR N-PSDB; ADA27374.  
XX  
XX New insect cell line designated ATCC PTA-4047, useful for replicating  
PT baculoviruses to produce large amounts of recombinant proteins of  
PT medical, pharmaceutical and veterinary importance.  
XX  
XX Disclosure; Page 59-60; 63pp; English.  
XX  
PS The present invention describes a cell line comprising a cell that is a  
CC clone, derivative, mutant and/or transfectant of a cell line designated  
CC American Type Culture Collection (ATCC) PTA-4047. The cell upon culture  
CC grows continuously and retains the identifying characteristics of the  
CC cell line designated ATCC-4047. Also described is a process of making a  
CC cell line. The insect cell line is useful in replicating baculoviruses,  
CC as a host substrate for baculovirus plaque assays, as a source of insect  
CC proteins, acts as a depot for cell transfection to produce recombinant  
CC baculoviruses, and in expressing viral recombinant proteins.  
CC Extracellular and intracellular viral recombinant proteins and virus-like  
CC particles expressed from the cell line are useful as pharmaceutical  
CC compositions, vaccines or diagnostic reagents. The present sequence  
CC represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion  
CC protein, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 805 AA:  
Query Match 99.2%; Score 513; DB 6; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56; Indels 0; Gaps 0;  
Matches 95; Conservative 0; Mismatches 3;  
QY 1 MHGDTPTLHEHYMDLOPETTDLYXXYXQINDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 60  
Db 471 MHGDTPTLHEHYMDLOPETTDLYGYEQINDSSEEDIDGPAGQAEPRRAHYNIIVTFCK 530  
QY 61 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98  
Db 531 CDSTLRICVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 568  
RESULT 8

ADA92544  
ID ADA92544 standard; protein; 805 AA.  
XX  
AC ADA92544;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion amino acid sequence SEQ ID NO:9.  
XX  
XX codon optimised; viral capsid protein; virus-like particle; VLP;  
KM antigenic; human papillomavirus infection; virucide; vaccine;  
KW gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;  
XX fusion protein.  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
XX MO2003068933-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004480.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
PI Robinson RA;  
XX  
XX WPI: 2003-689664/65.  
DR N-PSDB; ADA92552.  
XX  
XX New codon optimized polynucleotide encoding a viral capsid protein that  
PT self assembles into a virus-like particle, useful for diagnosing,  
PT preventing or treating human papillomavirus infections or associated  
PT disorders.  
XX  
XX Disclosure; Page 119-120; 123pp; English.  
PS  
XX  
XX The present invention describes a codon optimised polynucleotide encoding  
CC a viral capsid protein that self assembles into a virus-like particle  
CC (VLP) that exhibits conformational antigenic epitopes capable of raising  
CC neutralising antibodies, where the VLP is expressed from a host cell  
CC extracellularly. Also described: (1) a vector comprising the above codon  
CC optimised polynucleotide operably linked to a eukaryotic or prokaryotic  
CC regulatory control element, capable of replication in prokaryotic and/or  
CC eukaryotic host; (2) a host cell comprising the vector; (3) a  
CC pharmaceutical or vaccine composition for treating, ameliorating or  
CC preventing a papillomavirus related disease or disorder, comprising a  
CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and  
CC a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a  
CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit  
CC conformational antigenic epitopes, and a detection agent comprising a  
CC detectable label; (5) a method for preparing the above codon optimised  
CC polynucleotide, comprising replacing codons that are underutilised in  
CC insect cells with codons that are utilised at high levels in insect  
CC cells, to create an initially-modified nucleotide sequence, and modifying  
CC the initially-modified nucleotide sequence by choosing a preferred codon  
CC for the initially-modified sequence, where the ratio of GC nucleotide

CC pairs to AT nucleotide pairs in the further-modified nucleotide sequence  
CC trends towards about 1:1, where the number of palindromic and stem-loop  
CC DNA structures in the further-modified nucleotide sequence is minimised,  
CC and where the number of transcription and post-transcription repressor  
CC elements are minimised; and (6) methods for treating, ameliorating or  
CC preventing a papillomavirus related disease or disorder, or for  
CC protecting an individual against a papillomavirus infection, comprising  
CC administering to an individual an amount of the composition or vaccine  
CC cited above. The VLP has virucide activity and can be used in vaccines  
CC and in gene therapy. The composition and methods of the present invention  
CC are useful in diagnosing, preventing or treating human papillomavirus  
CC infections or associated disorders, such as dysplasia. The present  
CC sequence represents an HPV-16 codon optimised L2/E7/E2 fusion amino acid  
CC sequence from the present invention.  
XX  
XX  
SQ Sequence 805 AA;  
XX  
XX  
Query Match 99.2%; Score 513; DB 7; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEVYMLDQPEPTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITFCCK 60  
DB 471 MHGDTPTLHEVYMLDQPEPTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITFCCK 530  
QY 61 CDSTRLCVOSTHVDIRTLDELNGTIGIYXPCSQKP 98  
DB 531 CDSTRLCVOSTHVDIRTLDELNGTIGIYXPCSQKP 568  
RESULT 9  
ADA14293  
ID ADA14293 standard; protein; 805 AA.  
XX  
AC ADA14293;  
XX  
XX 06-NOV-2003 (first entry)  
XX  
DT HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.  
XX  
DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.  
XX  
KM purification; recombinant extracellular virus-like particle;  
KM recombinant intracellular virus-like particle; virus-like particle; VLP;  
KM virucide; vaccine; gene therapy; human papillomavirus; HPV; infection;  
KM dysplasia; HPV-16; fusion protein.  
XX  
XX  
OS Synthetic.  
OS Human papillomavirus type 16.  
XX  
XX WO2003068933-A1.  
XX  
XX 21-AUG-2003.  
XX  
PD 21-AUG-2003.  
XX  
XX 14-FEB-2003; 2003WO-US004474.  
XX  
XX 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.  
PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
XX (NOVA-) NOVAVAX INC.  
XX  
XX Robinson RA, Thompson MW;  
PI

XX WP1: 2003-679645/64.  
DR N-PSDB; ADA14301.  
XX  
PT Purifying a recombinant human papillomavirus (HPV) L1, useful for  
PT diagnosing, preventing or treating HPV infections, comprises clarifying,  
PT concentrating and diafiltering cells containing HPV particles.  
XX  
PS Disclosure; Page 103-104; 111pp; English.  
XX  
CC The present invention describes a method for purifying a recombinant  
CC extracellular or intracellular virus-like particle (VLP). The method  
CC comprises harvesting a cell suspension comprising cells containing a  
CC plurality of VLPs to produce a harvested supernatant, optionally  
CC disrupting the harvested cells to produce cell lysates containing the  
CC VLP, clarifying the harvested supernatant, concentrating the clarified  
CC supernatant, diafiltering the concentrated supernatant, and recovering  
CC the purified recombinant VLP. Also described: (1) a cell line designated  
CC as Sf-9S deposited as American Type Culture Collection (ATCC) PTA-4047;  
CC (2) producing the cell line described above; (3) host cells that express  
CC one or more recombinant gene products with an enhanced yield; (4)  
CC producing a foreign protein in an insect cell; (5) nucleic acid sequences  
CC that correspond to and code for human papillomavirus (HPV) polypeptides;  
CC and (6) pharmaceutical compositions comprising an amount of the  
CC recombinant viral gene products, VLPs, agonists, antagonists, or the  
CC active fragment of a viral gene product. The VLPs have virulence activity,  
CC and can be used in vaccines and in gene therapy. The method is useful in  
CC isolating and purifying expressed viral gene products, including VLPs, in  
CC vitro. The gene products or particles may be used in detecting,  
CC preventing or treating HPV infections and associated symptoms like  
CC dysplasia. The present sequence represents an HPV-16 L2/E7/E2 fusion  
CC protein, which is given in the exemplification of the present invention.  
XX  
SQ Sequence 805 AA:  
  
Query Match 99.2%; Score 513; DB 7; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MHGDTPTLHEYMLDLPETTTDLYXXQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 60  
DB 471 MHGDTPTLHEYMLDLPETTTDLYGYEQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 530  
  
QY 61 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 98  
DB 531 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 568  
  
RESULT 10  
AAE38618  
ID AAE38618 standard; protein; 805 AA.  
XX  
AC AAE38618;  
XX  
DT 04-DEC-2003 (first entry)  
XX  
DE HPV-16 L2/E7/E2 fusion protein.  
XX  
XX Vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV;  
KW virucide; papillomavirus infection; Human papillomavirus; fusion protein.  
XX  
OS Human papillomavirus.  
OS Synthetic.  
XX  
PN WO2003068163-A2.  
XX  
PD 21-AUG-2003.  
XX  
PF 14-FEB-2003; 2003WO-US004473.  
XX  
PR 14-FEB-2002; 2002US-0356113P.  
PR 14-FEB-2002; 2002US-0356118P.  
PR 14-FEB-2002; 2002US-0356119P.

PR 14-FEB-2002; 2002US-0356123P.  
PR 14-FEB-2002; 2002US-0356126P.  
PR 14-FEB-2002; 2002US-0356133P.  
PR 14-FEB-2002; 2002US-0356135P.  
PR 14-FEB-2002; 2002US-0356150P.  
PR 14-FEB-2002; 2002US-0356151P.  
PR 14-FEB-2002; 2002US-0356152P.  
PR 14-FEB-2002; 2002US-0356154P.  
PR 14-FEB-2002; 2002US-0356156P.  
PR 14-FEB-2002; 2002US-0356157P.  
PR 14-FEB-2002; 2002US-0356161P.  
PR 14-FEB-2002; 2002US-0356162P.  
XX  
PA (NOVA-) NOVAVAX INC.  
XX  
P1 Robinson RA, Cloce V;  
XX  
XX WP1: 2003-689598/65.  
DR N-PSDB; AAD58574.  
XX  
PT New chimeric virus-like particles comprising a recombinant viral capsid  
PT protein encapsulating a recombinant viral protein, useful for inducing  
PT humoral and/or cell-mediated immunity against papillomavirus infection.  
XX  
PS Disclosure; Page 122-123; 126pp; English.  
XX  
CC The present invention relates to chimeric virus-like particle comprising  
CC a recombinant viral capsid protein that encapsulates a recombinant viral  
CC protein during self assembly into a chimeric virus-like particle and  
CC exhibiting conformational antigenic epitopes capable of eliciting  
CC neutralising antibodies. The vaccine comprising the chimeric virus-like  
CC particles are useful for inducing immunity (humoral and/or cell-mediated  
CC immunity) against papillomavirus infection. The invention is also useful  
CC in gene therapy. The present sequence is HPV (human papillomavirus)-16  
CC L2/E7/E2 fusion protein  
XX  
SQ Sequence 805 AA:  
  
Query Match 99.2%; Score 513; DB 7; Length 805;  
Best Local Similarity 96.9%; Pred. No. 2.4e-56;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MHGDTPTLHEYMLDLPETTTDLYXXQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 60  
DB 471 MHGDTPTLHEYMLDLPETTTDLYGYEQLNDSSEEDIEDPAGQAEPRRAHYNIVTFCK 530  
  
QY 61 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 98  
DB 531 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 568  
  
RESULT 11  
AAR22767  
ID AAR22767 standard; peptide; 98 AA.  
XX  
AC AAR22767;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-SEP-1992 (first entry)  
XX  
DE HPV E7 peptide.  
XX  
KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9205248-A.  
XX  
PD 02-APR-1992.  
XX  
PF 26-SEP-1991; 91WO-US007081.  
XX



PR 26-SEP-1990; 90US-00588384.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL,  
XX WPI, 1992-132119/16.  
XX  
XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and  
PT recombinant cells encoding them, useful in treatment and prophylaxis of  
XX cervical warts or cancer resulting from HPV infection.  
XX  
XX Disclosure; Fig 7; 81pp; English.  
XX  
XX The peptide is the sequence of the human papillomavirus HPV 16 E7  
CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)  
CC of HPV 16 E7 were synthesized by standard Merrifield synthesis. Examples  
CC of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these  
CC peptides, antibodies against the peptides, or recombinant cells contg.  
CC the gene encoding the immunogenic peptides may be utilized in methods for  
CC inhibiting and treating HPV infection and tumour initiation and  
CC progression e.g. in the prevention or rebaration of cervical warts and  
CC cervical carcinoma resulting from HPV infection. See also AAR22766.  
CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to  
CC correct PI field.)  
XX  
XX Sequence 98 AA:  
SQ  
Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEWMLDQPEPTTDLVYXXQLNDSSEEDSIDGPAQAEPPRAHNYITFCCK 60  
DB 1 MHGDTPTLHEWMLDQPEPTTDLVYXXQLNDSSEEDSIDGPAQAEPPRAHNYITFCCK 60  
QY 61 CDSTRLCVOSTHVDIRLTEDLMGTGLIYVPICSQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLMGTGLIYVPICSQKP 98  
RESULT 12  
AAR42361  
ID AAR42361 standard; protein; 98 AA.  
XX  
XX AAR42361;  
AC  
XX 25-MAR-2003 (revised)  
DT 21-MAY-1994 (first entry)  
XX  
XX Human papillomavirus 16 E7 protein and fragments.  
DE  
XX Tumours; cows; horses; donkeys; regression; udder warts; HPV16.  
KM  
XX Synthetic.  
OS  
XX WO9320844-A1.  
PN  
XX 28-OCT-1993.  
PD  
XX 01-APR-1993; 93WO-GB000679.  
PF  
XX 08-APR-1992; 92GB-00007701.  
PR  
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.  
PA  
XX Camp MS;  
PI  
XX WPI; 1993-351368/44.  
DR  
XX Use of papilloma-virus E7 protein or fragments for the therapy of  
PT papilloma-virus disease - for the regression of tumours e.g. removal of  
PT warts from udders or mouth of milking cows or for treatment of horses or

PT donkeys.  
XX  
XX Disclosure; Fig 2; 31pp; English.  
XX  
XX The sequence is that of the human papillomavirus type 16 E7 protein. The  
CC protein sequence was aligned with that of bovine papillomavirus type 4.  
CC See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
XX Sequence 98 AA:  
SQ  
Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGDTPTLHEWMLDQPEPTTDLVYXXQLNDSSEEDSIDGPAQAEPPRAHNYITFCCK 60  
DB 1 MHGDTPTLHEWMLDQPEPTTDLVYXXQLNDSSEEDSIDGPAQAEPPRAHNYITFCCK 60  
QY 61 CDSTRLCVOSTHVDIRLTEDLMGTGLIYVPICSQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLMGTGLIYVPICSQKP 98  
RESULT 13  
AAW4686  
ID AAW4686 standard; protein; 98 AA.  
XX  
XX AAW4686;  
AC  
XX 25-MAR-2003 (revised)  
DT 15-JUN-1998 (first entry)  
XX  
XX Amino acid sequence of the HPV-16 E7 oncoprotein.  
DE  
XX E7 oncoprotein; proliferative state; HPV; kinase activity;  
XX cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;  
KM cyclin/cyclin-dependent kinase inhibitor.  
KW  
XX Human papillomavirus.  
OS  
XX US5736318-A.  
PN  
XX 07-APR-1998.  
PD  
XX 17-MAR-1995; 95US-00406248.  
PF  
XX 17-MAR-1995; 95US-00406248.  
PR  
XX 17-MAR-1995; 95US-00406248.  
PA (HARD ) UNIV HARVARD.  
XX (HARD ) HARVARD COLLEGE.  
XX  
XX Muenger K, Jones DL;  
PI  
XX WPI; 1998-239202/21.  
DR  
XX N-PSDB; AAV16717.  
XX  
XX Evaluation of proliferative state of cells transformed with human  
PT papilloma virus - by determining cyclin-dependent kinase activity induced  
PT by E7 onco-protein.  
XX  
XX Disclosure; Col 19-20; 14pp; English.  
XX  
XX The present sequence represents Human papillomavirus (HPV), strain 16, E7  
CC oncoprotein. The proliferative state of a cell transformed with HPV can  
CC be evaluated in the following manner. Cyclin/cyclin-dependent kinase  
CC complexes containing protein p21CIP1 (AAW4687-88) are isolated from the  
CC transformed cell, and the HPV E7 oncoprotein added to the isolated  
CC protein. Cyclin/cyclin-dependent kinase complexes are isolated from an  
CC untransformed cell that is substantially homologous with the transformed  
CC cell, and the HPV E7 oncoprotein added. The kinase activities of the 2  
CC samples are measured, where a proliferating transformed cell has a  
CC greater kinase activity than the untransformed cell. The method is used  
CC for determining the extent of interaction and/or inactivation between a

CC Cyclic/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and  
CC thus evaluating the proliferative state of a transformed cell. (Updated  
CC on 25-MAR-2003 to correct PI field.)

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 2; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 MGGDTPLHEHYMLDLPETTDLYXXQLNDSSEDEIDGPAGAPDPRAHNYIVTFCK 60

1 MGGDTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGAPDPRAHNYIVTFCK 60

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

CC also be used to generate resistance to bacterial or viral damage.  
CC Sequences AA58472-Y58474 represent examples of viral proteins which  
CC affect proteasomal function

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 MGGDTPLHEHYMLDLPETTDLYXXQLNDSSEDEIDGPAGAPDPRAHNYIVTFCK 60

1 MGGDTPLHEHYMLDLPETTDLYCYEQLNDSSEDEIDGPAGAPDPRAHNYIVTFCK 60

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

61 CDSTLRLCVOSTHVDIRLTEDLMTGLGIXPICSQKP 98

Best Local Similarity 96.9%; Pred. No. 2.2e-57;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

OY		61	CSTLRVCQSHVDIRTLBLLMGTLGIXPICSQKP	98
Dd		61	CSTLRVCQSHVDIRTLBLLMGTLGIXPICSQKP	98

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Job time : 146.655 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:11:25 ; Search time 28.7309 Seconds  
(without alignments)  
298.563 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517  
Sequence: 1 MHGDPPTLHEFMLDQPERTT.....LEDLLMGTGLGVPCISQKP 98

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents AA.\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	99.2	220	2	US-09-485-885-8
2	512	99.0	98	1	US-08-406-248-6
3	512	99.0	98	2	US-08-075-541D-42
4	512	99.0	98	2	US-09-382-616A-1
5	512	99.0	98	2	US-08-944-368A-4
6	512	99.0	98	2	US-09-820-764-4
7	512	99.0	98	2	US-09-986-118A-4
8	512	99.0	98	2	US-09-728-466-1
9	512	99.0	98	2	US-09-824-017-4
10	512	99.0	98	2	US-09-637-746-3
11	512	99.0	98	2	US-09-501-097A-7
12	512	99.0	98	2	US-09-980-523A-12
13	512	99.0	121	2	US-09-613-303-12
14	512	99.0	121	2	US-10-267-311-12
15	512	99.0	198	2	US-09-613-303-35
16	512	99.0	198	2	US-10-267-311-35
17	512	99.0	220	2	US-09-485-885-1
18	512	99.0	239	2	US-09-485-885-12
19	512	99.0	253	1	US-08-459-818-20
20	512	99.0	253	1	US-08-889-666-20
21	512	99.0	253	1	US-08-465-078-20
22	512	99.0	253	1	US-08-725-776-20
23	512	99.0	253	1	US-08-488-062-20
24	512	99.0	266	1	US-08-117-083-9
25	512	99.0	266	2	US-08-860-165-10
26	512	99.0	266	2	US-09-359-382-10

27	512	99.0	266	2	US-09-367-309A-1	Sequence 1, Appli
28	512	99.0	287	2	US-09-501-097A-25	Sequence 25, Appli
29	512	99.0	295	2	US-09-613-303-33	Sequence 33, Appli
30	512	99.0	295	2	US-10-267-311-33	Sequence 33, Appli
31	512	99.0	324	2	US-09-613-303-25	Sequence 25, Appli
32	512	99.0	324	2	US-10-267-311-25	Sequence 25, Appli
33	512	99.0	371	2	US-09-485-885-6	Sequence 6, Appli
34	512	99.0	390	2	US-09-485-885-14	Sequence 14, Appli
35	512	99.0	493	2	US-09-613-303-19	Sequence 19, Appli
36	512	99.0	493	2	US-10-267-311-19	Sequence 19, Appli
37	512	99.0	639	2	US-09-613-303-17	Sequence 17, Appli
38	512	99.0	639	2	US-10-267-311-17	Sequence 17, Appli
39	512	99.0	641	2	US-09-613-303-51	Sequence 51, Appli
40	512	99.0	641	2	US-10-267-311-51	Sequence 51, Appli
41	512	99.0	647	2	US-09-613-303-53	Sequence 53, Appli
42	512	99.0	647	2	US-10-267-311-53	Sequence 53, Appli
43	507	98.1	98	2	US-09-566-420-19	Sequence 19, Appli
44	507	98.1	98	2	US-10-201-764-19	Sequence 19, Appli
45	503	97.3	98	2	US-09-613-303-8	Sequence 8, Appli

## ALIGNMENTS

```
RESULT 1
US-09-485-885-8
; Sequence 8, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchelkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-8

Query Match          99.2% Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 1.8e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 MHGDPPTLHEFMLDQPERTTLYXXOINDSEEDERIDGAGQAEPRAHNYITFFCK 60
        |||||
DB      114 MHGDPPTLHEFMLDQPERTTLYGQOINDSEEDERIDGAGQAEPRAHNYITFFCK 173
        |||||
        61 CDSTRLCVGOSTHVDIRTLDELMLGTGLGVPCISQKP 98
        |||||
        174 CDSTRLCVGOSTHVDIRTLDELMLGTGLGVPCISQKP 211

RESULT 2
US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Ann-Louise Kerner, Ph.D., Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDanielis, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1311
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-248-6

Query Match          99.0%; Score 512; DB 1; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98

RESULT 3
US-08-075-541D-42
Sequence 42, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESS: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
```

```

FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match          99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98

RESULT 4
US-09-382-616A-1
Sequence 1, Application US/09382616A
Patent No. 6200746
GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Manxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match          99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEYMLDLPETTDLYXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLYCYEQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRLTEDLMLGTGLGVXPCISQKP 98

RESULT 5
US-08-944-368A-4
Sequence 4, Application US/08944368A
Patent No. 6228368
GENERAL INFORMATION:
APPLICANT: Gissman, et al.
```

TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine  
NUMBER OF INVENTION: Formulations and Methods of Use  
CORRESPONDENCE ADDRESSES: 28  
ADDRESS: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 233 South Wacker Drive, 6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,368A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.  
REGISTRATION NUMBER: 38,659  
REFERENCE/DOCKET NUMBER: 27013/34028  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-944-368A-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYQUNDSEEDIEDGPAQAEPRAHNYITFPCK 60  
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSEEDIEDGPAQAEPRAHNYITFPCK 60  
Qy 61 CDSTRLCVOSTHVDIRTELDLMTGLGIVPICGQKP 98  
Db 61 CDSTRLCVOSTHVDIRTELDLMTGLGIVPICGQKP 98

RESULT 6  
US-09-820-764-4  
Sequence 4, Application US/09920764  
Patent No. 6352696  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/820,764  
FILING DATE: 30-Mar-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: 20-FEB-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Collin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-820-764-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYQUNDSEEDIEDGPAQAEPRAHNYITFPCK 60  
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSEEDIEDGPAQAEPRAHNYITFPCK 60  
Qy 61 CDSTRLCVOSTHVDIRTELDLMTGLGIVPICGQKP 98  
Db 61 CDSTRLCVOSTHVDIRTELDLMTGLGIVPICGQKP 98

RESULT 7  
US-09-986-118A-4  
Sequence 4, Application US/09986118A  
Patent No. 6562351  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,118A  
FILING DATE: 07-No. 6562351-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Collin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98  
DB 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98

RESULT 8  
US-09-728-466-1

Sequence 1, Application US/09728466  
Patent No. 6641994  
GENERAL INFORMATION:  
APPLICANT: Fisher, Christopher  
APPLICANT: He, Manxia  
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents  
FILE REFERENCE: 28341/6216  
CURRENT APPLICATION NUMBER: US/09/728,466  
CURRENT FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: 09/382,616  
PRIOR FILING DATE: 1999-08-25  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Papillomavirus sylvilagi  
US-09-728-466-1

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98  
DB 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98

RESULT 9  
US-09-824-017-4

Sequence 4, Application US/09824017  
Patent No. 6649167  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
APPLICANT: HALLER, Michael  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-Apr-2001  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-824-017-4

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98  
DB 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98

RESULT 10

US-09-637-746-3  
Sequence 3, Application US/09637746  
Patent No. 6727079  
GENERAL INFORMATION:  
APPLICANT: Thorgeirsson, Snorri S.  
APPLICANT: Moltach, Joseph T.  
APPLICANT: Zhang, Minghuang  
TITLE OF INVENTION: CDNA ENCODING A GENE BOG (BET OVER-EXPRESSED GENE) AND ITS PROTEIN  
FILE REFERENCE: 11613.29USW1  
CURRENT APPLICATION NUMBER: US/09/637,746  
CURRENT FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: PCT/US99/04142  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: US 60/079,567  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/075,922  
PRIOR FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-09-637-746-3

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98  
QY 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTIGIVPCISQKP 98



Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 11  
US-09-501-097A-7  
; Sequence 7, Application US/09501097A  
; Patent No. 6734173  
; GENERAL INFORMATION:  
; APPLICANT: Tzyy-Chou Wu  
; APPLICANT: Chien-Fu Hung  
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES  
; FILE REFERENCE: 2240-169349  
; CURRENT APPLICATION NUMBER: US/09/501,097A  
; PRIORITY FILING DATE: 2000-02-09  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: human papillomavirus  
US-09-501-097A-7

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEYMLDQPEPTDLYCYEQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 12  
US-09-980-523A-12  
; Sequence 12, Application US/09980523A  
; Patent No. 6783763  
; GENERAL INFORMATION:  
; APPLICANT: CHOPPIN, JEANNINE  
; APPLICANT: BOURGAULT VILLADA, ISABELLE  
; APPLICANT: GUILLET, JEAN-GERARD  
; APPLICANT: CONNAN, FRANCINE  
; APPLICANT: FERRIERES, ESTELLE  
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
; FILE REFERENCE: WO81 AO INS  
; CURRENT APPLICATION NUMBER: US/09/980,523A  
; PRIORITY FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: PCT/FR00/01513  
; PRIORITY FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: FR 99/07012  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Human Papillomavirus  
US-09-980-523A-12

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 8e-60;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 1 MHGDTPLHEYMLDQPEPTDLYCYEQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 13  
US-09-613-303-12  
; Sequence 12, Application US/09613303  
; Patent No. 6495347  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/09/613,303  
; PRIORITY FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIORITY FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-09-613-303-12

Query Match 99.0%; Score 512; DB 2; Length 121;  
Best Local Similarity 96.9%; Pred. No. 1.1e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60  
Db 24 MHGDTPLHEYMLDQPEPTDLYCYEQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 83

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98  
Db 84 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 121

RESULT 14  
US-10-267-311-12  
; Sequence 12, Application US/10267311  
; Patent No. 6657055  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Marvin  
; APPLICANT: Chu, N. Randall  
; APPLICANT: Mizzen, Lee A.  
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO  
; FILE REFERENCE: 12071/002001  
; CURRENT APPLICATION NUMBER: US/10/267,311  
; PRIORITY FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US/09/613,303  
; PRIORITY FILING DATE: 2000-07-10  
; PRIOR APPLICATION NUMBER: US 60/143,757  
; PRIORITY FILING DATE: 1999-07-08  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: fusion sequence  
US-10-267-311-12

Query Match 99.0%; Score 512; DB 2; Length 121;  
Best Local Similarity 96.9%; Pred. No. 1.1e-59;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXYXQUNDSEDEIDGPAGQAEPPRAHYNIVTFCK 60

Db 24 MHGDTPTLHEYMLDLPETTDLYCYEQINDSSEDEIDGPAGQAEPRRAHYNIVTFCK 83

QY 61 CDSTLRLCVQSTHVDIRTLIEDLGMGTGIVXPICQKP 98

Db 84 CDSTLRLCVQSTHVDIRTLIEDLGMGTGIVXPICQKP 121

RESULT 15

US-09-613-303-35  
; Sequence 35, Application US/09613303  
; Patent No. 6495347

; GENERAL INFORMATION:

; APPLICANT: Siegel, Marvin

; APPLICANT: Chu, N. Randall

; APPLICANT: Mizen, Lee A.

; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

; FILE REFERENCE: 12071/002001

; CURRENT APPLICATION NUMBER: US/09/613,303

; PRIOR FILING DATE: 2000-07-10

; PRIOR APPLICATION NUMBER: US 60/143,757

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 198

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: fusion sequence

US-09-613-303-35

Query Match 99.0%; Score 512; DB 2; Length 198;

Best Local Similarity 96.9%; Pred. No. 2.1e-59;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPETTDLYXXYXQINDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60

Db 101 MHGDTPTLHEYMLDLPETTDLYCYEQINDSSEDEIDGPAGQAEPRRAHYNIVTFCK 160

QY 61 CDSTLRLCVQSTHVDIRTLIEDLGMGTGIVXPICQKP 98

Db 161 CDSTLRLCVQSTHVDIRTLIEDLGMGTGIVXPICQKP 198

Search completed: June 6, 2006, 12:13:13  
Job time : 29.7309 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:10 ; Search time 106.659 Seconds  
(without alignments)  
425.611 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517

Sequence: 1 MHGDPPTLHEFMLDLPETT.....LEDLLMGTLGIVPICSQKP 98

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	5	US-10-530-253-11 Sequence 11, Appl
2	513	99.2	220	4	US-10-000-903-8 Sequence 8, Appl
3	513	99.2	220	5	US-10-899-771-8 Sequence 8, Appl
4	513	99.2	248	5	US-10-530-253-9 Sequence 9, Appl
5	513	99.2	805	4	US-10-367-095-9 Sequence 9, Appl
6	513	99.2	805	4	US-10-368-046-9 Sequence 9, Appl
7	513	99.2	805	4	US-10-367-367-9 Sequence 9, Appl
8	513	99.2	805	5	US-10-918-337-9 Sequence 9, Appl
9	512	99.0	98	3	US-09-728-466-1 Sequence 1, Appl
10	512	99.0	98	3	US-09-820-765-4 Sequence 4, Appl
11	512	99.0	98	3	US-09-824-017-4 Sequence 4, Appl
12	512	99.0	98	3	US-09-986-118A-4 Sequence 4, Appl
13	512	99.0	98	3	US-10-177-390-8 Sequence 8, Appl
14	512	99.0	98	4	US-10-654-129-4 Sequence 4, Appl
15	512	99.0	98	4	US-10-772-988-3 Sequence 3, Appl
16	512	99.0	98	4	US-10-479-541-5 Sequence 5, Appl
17	512	99.0	98	5	US-10-042-526A-4 Sequence 4, Appl
18	512	99.0	98	5	US-10-657-399-1 Sequence 1, Appl
19	512	99.0	98	5	US-10-858-384-12 Sequence 12, Appl
20	512	99.0	98	5	US-10-343-448-5 Sequence 5, Appl
21	512	99.0	98	5	US-10-367-057-17 Sequence 17, Appl
22	512	99.0	98	5	US-10-530-253-14 Sequence 14, Appl
23	512	99.0	98	6	US-11-077-939-5 Sequence 5, Appl
24	512	99.0	98	6	US-11-179-478-4 Sequence 4, Appl
25	512	99.0	121	4	US-10-267-311-12 Sequence 12, Appl
26	512	99.0	121	5	US-10-679-956-12 Sequence 12, Appl
27	512	99.0	198	4	US-10-267-311-35 Sequence 35, Appl

28	512	99.0	198	5	US-10-679-956-35 Sequence 35, Appl
29	512	99.0	220	4	US-10-000-903-1 Sequence 1, Appl
30	512	99.0	220	5	US-10-899-771-1 Sequence 1, Appl
31	512	99.0	239	4	US-10-000-903-12 Sequence 12, Appl
32	512	99.0	239	5	US-10-899-771-12 Sequence 12, Appl
33	512	99.0	248	5	US-10-530-253-7 Sequence 7, Appl
34	512	99.0	256	6	US-11-192-923A-2 Sequence 2, Appl
35	512	99.0	266	3	US-09-367-309A-1 Sequence 1, Appl
36	512	99.0	295	4	US-10-267-311-33 Sequence 33, Appl
37	512	99.0	295	5	US-10-679-956-33 Sequence 33, Appl
38	512	99.0	324	4	US-10-267-311-25 Sequence 25, Appl
39	512	99.0	324	5	US-10-679-956-25 Sequence 25, Appl
40	512	99.0	334	4	US-10-472-724-10 Sequence 10, Appl
41	512	99.0	371	4	US-10-000-903-6 Sequence 6, Appl
42	512	99.0	371	5	US-10-899-771-6 Sequence 6, Appl
43	512	99.0	390	4	US-10-000-903-14 Sequence 14, Appl
44	512	99.0	390	5	US-10-899-771-14 Sequence 14, Appl
45	512	99.0	421	4	US-10-266-770-7 Sequence 7, Appl

## ALIGNMENTS

```
RESULT 1
US-10-530-253-11
; Sequence 11, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffery K. Pullen
; APPLICANT: Susan F. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530, 253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415, 929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-11
Query Match      99.4%; Score 514; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 3.3e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEFMLDLPETTLDYXXYXOLDSSSEDEIDGPAQAEPRAHYNIYTFCK 60
        |||||||
DB      1 MHGDPPTLHEFMLDLPETTLDYXXYXOLDSSSEDEIDGPAQAEPRAHYNIYTFCK 60
        |||||||
        61 CDSTLRICVQSTHVDIRTLEDLLMGTLGIVPICSQKP 98
        |||||||
        61 CDSTLRICVQSTHVDIRTLEDLLMGTLGIVPICSQKP 98
        |||||||
RESULT 2
US-10-000-903-8
; Sequence 8, Application US/10000903
; Publication No. US2002018221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Tereesa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Chislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
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;; CURRENT APPLICATION NUMBER: US/10/000,903  
;; CURRENT FILING DATE: 2001-10-01  
;; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
;; PRIOR FILING DATE: 1998-08-17  
;; PRIOR APPLICATION NUMBER: GB 9717953.5  
;; PRIOR FILING DATE: 1997-08-22  
;; NUMBER OF SEQ ID NOS: 23  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8  
;; LENGTH: 220  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
US-10-000-903-8

Query Match 99.2%; Score 513; DB 4; Length 220;  
Best Local Similarity 96.9%; Pred. No. 3,8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60  
Db 114 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 173

Qy 61 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 98  
Db 174 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYCPICSQKP 211

RESULT 3  
US-10-899-771-8  
; Sequence 8, Application US/10899771  
; Publication No. US20050031638A1  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/10/899,771  
; CURRENT FILING DATE: 2004-07-27  
; PRIOR APPLICATION NUMBER: US/09/581,976  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-10-899-771-8

US-10-899-771-8

Query Match 99.2%; Score 513; DB 5; Length 220;  
Best Local Similarity 96.9%; Pred. No. 3,8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60  
Db 114 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 173

Qy 61 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 98  
Db 174 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYCPICSQKP 211

RESULT 4  
US-10-530-253-9  
; Sequence 9, Application US/10530253

;; Publication No. US20060014926A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Casaretti, Maria C.  
;; APPLICANT: Smith, Larry  
;; APPLICANT: Jeffrey K. Pullen  
;; APPLICANT: Susan P. McElhinney  
;; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
;; FILE REFERENCE: 00630/100M137-US2  
;; CURRENT APPLICATION NUMBER: US/10/530,253  
;; CURRENT FILING DATE: 2005-04-04  
;; PRIOR APPLICATION NUMBER: PCT/US2003/031726  
;; PRIOR FILING DATE: 2003-10-02  
;; PRIOR APPLICATION NUMBER: US 60/415,929  
;; PRIOR FILING DATE: 2002-10-03  
;; NUMBER OF SEQ ID NOS: 65  
;; SOFTWARE: Patentn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 248  
;; TYPE: PRT  
;; ORGANISM: Human papillomavirus type 16  
US-10-530-253-9

Query Match 99.2%; Score 513; DB 5; Length 248;  
Best Local Similarity 96.9%; Pred. No. 4,4e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60  
Db 1 MHGDPPTLHEMYLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60

Qy 61 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYXPCSQKP 98  
Db 61 CDSTLRFCVQSTHVDIRLTEDLMLGTLGIYCPICSQKP 98

RESULT 5  
US-10-367-095-9  
; Sequence 9, Application US/10367095  
; Publication No. US20030228696A1  
; GENERAL INFORMATION:  
; APPLICANT: Robin A. Robinson  
; TITLE OF INVENTION: No. US20030228696A1 Insect Cell Line  
; FILE REFERENCE: 44149-1US1  
; CURRENT APPLICATION NUMBER: US/10/367,095  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,119  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,161  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,118  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,133  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,157  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,156  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,123  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,113  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,154  
; PRIOR FILING DATE: 2002-02-14  
; PRIOR APPLICATION NUMBER: US 60/356,135  
; PRIOR FILING DATE: 2002-02-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 805  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

US-10-367-095-9

OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein  
US-10-367-095-9

Query Match 99.2%; Score 513; DB 4; Length 805;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 60  
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 98  
Db 531 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 568

RESULT 6  
US-10-368-046-9

Sequence 9, Application US/10368046  
Publication No. US20040063188A1

GENERAL INFORMATION:

APPLICANT: Robin A. Robinson

APPLICANT: Vitoria Cioce

TITLE OF INVENTION: Method for Isolation and Purification of

FILE REFERENCE: 44149-3U51

CURRENT APPLICATION NUMBER: US/10/368,046

PRIOR FILING DATE: 2003-02-15

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,123

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,154

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,135

PRIOR FILING DATE: 2002-02-14  
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 805

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein

Query Match 99.2%; Score 513; DB 4; Length 805;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 60  
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 98  
Db 531 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 568

RESULT 7

US-10-367-367-9  
Sequence 9, Application US/10367367  
Publication No. US20040121465A1

GENERAL INFORMATION:

APPLICANT: Robin A. Robinson

TITLE OF INVENTION: Optimization of Gene Sequences of

FILE REFERENCE: 44149-2U51

CURRENT APPLICATION NUMBER: US/10/367,367

PRIOR FILING DATE: 2003-02-15

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 805

TYPE: PRT

ORGANISM: Artificial Sequence

OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein

Query Match 99.2%; Score 513; DB 4; Length 805;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 60  
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQXNDSESEDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 98  
Db 531 CDSTRLCVQSTHVDIRLTEDLMLGTLGIVPCISQKP 568

RESULT 8  
US-10-918-337-9

Sequence 9, Application US/10918337  
Publication No. US20050118191A1

GENERAL INFORMATION:

APPLICANT: NOVAVAX, INC., et al.

TITLE OF INVENTION: Optimization of Gene Sequences of

FILE REFERENCE: 19065/2132

CURRENT APPLICATION NUMBER: US/10/918,337

PRIOR FILING DATE: 2004-08-13

PRIOR APPLICATION NUMBER: PCT/US03/04473

PRIOR FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,123

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR FILING DATE: 2002-02-14  
PRIOR APPLICATION NUMBER: US 60/356,154  
PRIOR FILING DATE: 2002-02-14  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 9  
LENGTH: 805  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein  
US-10-918-337-9

Query Match 99.2%; Score 513; DB 5; Length 805;  
Best Local Similarity 96.9%; Pred. No. 1.9e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 60  
Db 471 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 530

Qy 61 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 98  
Db 531 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 568

RESULT 9  
US-09-728-466-1

Sequence 1, Application US/09728466  
Patent No. US20010029022A1

GENERAL INFORMATION:

APPLICANT: Fisher, Christopher

TITLE OF INVENTION: Methods to Identify Anti-Viral Agents

FILE REFERENCE: 28341/6216

CURRENT APPLICATION NUMBER: US/09/728,466

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: 09/382,616

PRIOR FILING DATE: 1999-08-25

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1

LENGTH: 98

TYPE: PRT

ORGANISM: Papillomavirus sv1v1agi

US-09-728-466-1

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 60  
Db 1 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 98  
Db 61 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 98

RESULT 10  
US-09-820-765-4

Sequence 4, Application US/09820765  
Publication No. US20020039584A1

GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

HALLEK, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,765

FILING DATE: 30-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/026,896

FILING DATE: 20-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Sandercock, Colin G.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37067/102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 98 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 60  
Db 1 MHGDTPLHEWMLDQPTTDLXXYXQUNDSEDEIDGPAGQAPDRAHNYIVTFCK 60

Qy 61 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 98  
Db 61 CDSTLRFCVOSTHVDIRTLMDLMTGLGIYXPCISQKP 98

RESULT 11  
US-09-824-017-4

Sequence 4, Application US/09824017  
Publication No. US20020197668A1

GENERAL INFORMATION:

APPLICANT: BURGER, Alexander

HALLEK, Michael

TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

FORMULATIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-824-017-4

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETPTDLYXXQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60  
Db 1 MHGDTPTLHEYMLDLPETPTDLYCYEQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 12  
US-09-986-118A-4  
Sequence 4, Application US/09986118A  
Publication No. US20030021806A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/986,118A  
FILING DATE: 07-NO. US20030021806A1-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/026,896  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 3; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETPTDLYXXQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60  
Db 1 MHGDTPTLHEYMLDLPETPTDLYCYEQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 13  
US-10-177-390-8  
Sequence 8, Application US/10177390  
Publication No. US20030143743A1  
GENERAL INFORMATION:  
APPLICANT: Schuler, Gerold  
APPLICANT: N.V. Antwerpse Innovatiecentrum  
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear  
FILE REFERENCE: 021505wo/0h/ml  
CURRENT APPLICATION NUMBER: US/10/177,390  
CURRENT FILING DATE: 2002-06-20  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURES:  
OTHER INFORMATION: Description of Artificial Sequence: fragment of  
US-10-177-390-8

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETPTDLYXXQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60  
Db 1 MHGDTPTLHEYMLDLPETPTDLYCYEQLNDSSEDEIDGPAGQAPDRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98  
Db 61 CDSTRLCVOSTHVDIRLTEDLMLGTLGIYVPCISQKP 98

RESULT 14  
US-10-654-129-4  
Sequence 4, Application US/10654129  
Publication No. US20040081661A1  
GENERAL INFORMATION:  
APPLICANT: BURGER, Alexander  
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE  
FORMULATIONS AND METHODS OF USE  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/654,129  
FILING DATE: 04-Sep-2003  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/824,017  
FILING DATE: 03-Apr-2001  
APPLICATION NUMBER: 09/026,896  
FILING DATE: 1998-02-20  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37067/102  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 98 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-654-129-4

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGQAEPRAHYNIYTFCK 60  
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60

Qy 61 CDSTLRLCVQSTHVDIRLTEDLMGTLGIVXPICQKP 98  
Db 61 CDSTLRLCVQSTHVDIRLTEDLMGTLGIVCPICQKP 98

RESULT 15  
US-10-772-988-3  
Sequence 3, Application US/10772988  
Publication No. US20040139485A1  
GENERAL INFORMATION:  
APPLICANT: Thorigeitson, Snorri S.  
APPLICANT: Woltach, Joseph T.  
TITLE OF INVENTION: CDNA ENCODING A GENE BOG (B5T OVER-EXPRESSED GENE) AND ITS PROTEIN  
FILE REFERENCE: 11613.29USW1  
CURRENT APPLICATION NUMBER: US/10/772,988  
CURRENT FILING DATE: 2004-02-05  
PRIOR APPLICATION NUMBER: US/09/637,746  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: PCT/US99/04142  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: US 60/079,567  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: US 60/075,922  
PRIOR FILING DATE: 1998-02-25  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 98  
TYPE: PRT  
ORGANISM: Human papillomavirus  
US-10-772-988-3

Query Match 99.0%; Score 512; DB 4; Length 98;  
Best Local Similarity 96.9%; Pred. No. 1.8e-53;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGQAEPRAHYNIYTFCK 60

Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPRAHYNIYTFCK 60  
Qy 61 CDSTLRLCVQSTHVDIRLTEDLMGTLGIVXPICQKP 98  
Db 61 CDSTLRLCVQSTHVDIRLTEDLMGTLGIVCPICQKP 98

Search completed: June 6, 2006, 12:32:59  
Job time : 107.659 secs



GenCore version 5.1.9  
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## OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:35 ; Search time 7.08434 Seconds

(without alignment)  
159.985 Million cell updates/sec

Title: US-10-530-253-14

Sequence: 1 MHGPTTHHEYMLDQPEPTT.....LEDLMGTGIVPCISQKP 98

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

1: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US09\_NEW\_PUB.pep.\*  
2: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US06\_NEW\_PUB.pep.\*  
3: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US07\_NEW\_PUB.pep.\*  
4: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US08\_NEW\_PUB.pep.\*  
5: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/PCr\_NEW\_PUB.pep.\*  
6: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US11\_NEW\_PUB.pep.\*  
7: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US11\_NEW\_PUB.pep.\*  
8: /EMC\_Celerra\_SIDS3/ptodate/2/pubppaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	US-10-511-814-8	Sequence 8, Appli
2	511	98.8	98	US-10-511-814-11	Sequence 11, Appli
3	478	92.5	92	US-10-512-190-2	Sequence 2, Appli
4	102	19.7	21	US-11-209-206-6	Sequence 6, Appli
5	80.5	15.6	21	US-11-209-206-7	Sequence 7, Appli
6	62.5	12.1	148	US-11-293-697-2678	Sequence 2678, Ap
7	60.5	11.7	1287	US-10-505-928-341	Sequence 341, App
8	60	11.6	468	US-11-293-697-4473	Sequence 4473, App
9	58.5	11.3	462	US-10-953-349-39521	Sequence 39521, A
10	58.5	11.3	616	US-10-953-349-39520	Sequence 39520, A
11	58.5	11.3	646	US-10-953-349-39519	Sequence 39519, A
12	57.5	11.1	233	US-10-953-349-27426	Sequence 27426, A
13	57.5	11.1	296	US-10-953-349-27425	Sequence 27425, A
14	57.5	11.1	353	US-10-953-349-27424	Sequence 27424, A
15	57.5	11.1	446	US-10-953-349-39537	Sequence 39537, A
16	57.5	11.1	464	US-10-953-349-39536	Sequence 39536, A
17	57.5	11.1	499	US-10-953-349-3781	Sequence 3781, Ap
18	57.5	11.1	552	US-10-953-349-3780	Sequence 3780, Ap
19	57.5	11.1	618	US-10-953-349-39535	Sequence 39535, A
20	57	11.0	300	US-11-242-111-23	Sequence 23, Appli
21	57	11.0	314	US-09-981-845-1	Sequence 1, Appli
22	55.5	10.7	286	US-10-953-349-23406	Sequence 23406, A
23	55.5	10.7	293	US-10-953-349-23405	Sequence 23405, A
24	55.5	10.7	538	US-10-953-349-5452	Sequence 5452, Ap
25	55.5	10.7	544	US-10-953-349-5451	Sequence 5451, Ap

26	55.5	10.7	574	US-10-953-349-5450	Sequence 5450, Ap
27	55.5	10.7	878	US-10-468-193-32	Sequence 32, Appli
28	54.5	10.5	58	US-10-525-126-177	Sequence 177, App
29	54.5	10.5	58	US-10-525-126-215	Sequence 215, App
30	54.5	10.5	88	US-10-525-126-175	Sequence 175, App
31	54.5	10.5	88	US-10-525-126-174	Sequence 174, App
32	54.5	10.5	88	US-10-525-126-212	Sequence 212, App
33	54.5	10.5	88	US-10-525-126-213	Sequence 213, App
34	54.5	10.5	88	US-10-525-126-284	Sequence 284, App
35	54.5	10.5	88	US-10-525-126-299	Sequence 299, App
36	54.5	10.5	88	US-10-525-126-300	Sequence 300, App
37	54.5	10.5	255	US-10-953-349-20549	Sequence 20549, A
38	54.5	10.5	269	US-10-953-349-20548	Sequence 20548, A
39	54.5	10.5	489	US-11-293-697-2988	Sequence 2988, A
40	54	10.4	278	US-10-953-349-1526	Sequence 1526, App
41	54	10.4	323	US-10-518-414-1	Sequence 1, Appli
42	54	10.4	630	US-10-953-349-35808	Sequence 35808, A
43	54	10.4	676	US-10-953-349-35807	Sequence 35807, A
44	53.5	10.3	533	US-10-953-349-31198	Sequence 31198, A
45	53.5	10.3	639	US-10-953-349-23351	Sequence 23351, A

## ALIGNMENTS

RESULT 1  
US-10-511-814-8  
; Sequence 8, Application US/10511814  
; Publication No. US20060088472A1  
; GENERAL INFORMATION:  
; APPLICANT: Mccance, Dennis  
; APPLICANT: Westbrook, Ili, Thomas F.  
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT  
; FILE REFERENCE: 21108.0016U2  
; CURRENT APPLICATION NUMBER: US/10/511,814  
; PRIOR FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US03/12667  
; PRIOR FILING DATE: 2003-04-21  
; PRIOR APPLICATION NUMBER: 60/374,245  
; PRIOR FILING DATE: 2002-04-19  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence./Note =  
US-10-511-814-8  
Query Match 99.0%; Score 512; DB 6; Length 98;  
Best Local Similarity 96.9%; Pred. No. 2.4e-50;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MHGPTTHHEYMLDQPEPTTLLYXXQUNDSEBDEIDGAGQAEPPRAHNYITPCK 60  
DB 1 MHGPTTHHEYMLDQPEPTTLLYXXQUNDSEBDEIDGAGQAEPPRAHNYITPCK 60  
QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTTGIVPCISQKP 98  
DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTTGIVPCISQKP 98  
RESULT 2  
US-10-511-814-11  
; Sequence 11, Application US/10511814  
; Publication No. US20060088472A1  
; GENERAL INFORMATION:  
; APPLICANT: Mccance, Dennis  
; APPLICANT: Westbrook, Ili, Thomas F.  
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT  
; FILE REFERENCE: 21108.0016U2

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; CURRENT APPLICATION NUMBER: US/10/511,814
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
US-10-511-814-11

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Query Match          98.8%; Score 511; DB 6; Length 98;
Best Local Similarity 95.9%; Pred. No. 3.1e-50;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPDRAHNYITVFCCK 60
Db      1 MHGDPPTLHEYMLDLPETTDLYCYEQLNDSSEEDRIDGPAQAEPDRAHNYITVFCCK 60
Qy      61 CDSTLRLCVOSTHVDIRTLBLLMGTGIVYPCISQKP 98
Db      61 CDSTLRLCVOSTHVDIRTLBLLMGTGIVYPCISQKP 98

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RESULT 3
US-10-512-190-2
; Sequence 2, Application US/10512190
; Publication No. US20060099219A1
; GENERAL INFORMATION:
; APPLICANT: Hallee, Sophie
; APPLICANT: Burny, Arsene
; APPLICANT: Jacquet, Alain
; TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
; FILE REFERENCE: 9997.50USMO
; CURRENT APPLICATION NUMBER: US/10/512,190
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/BE03/000073
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/410,461
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: FR 0205173
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: FR 03041170
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
US-10-512-190-2

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Query Match          92.5%; Score 478; DB 6; Length 92;
Best Local Similarity 92.9%; Pred. No. 1.3e-46;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

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Qy      1 MHGDPPTLHEYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPDRAHNYITVFCCK 60
Db      1 MHGDPPTLHEYMLDLPETT-----QNDSSSEEDRIDGPAQAEPDRAHNYITVFCCK 54
Qy      61 CDSTLRLCVOSTHVDIRTLBLLMGTGIVYPCISQKP 98
Db      55 CDSTLRLCVOSTHVDIRTLBLLMGTGIVYPCISQKP 92

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RESULT 4
US-11-209-206-6
; Sequence 6, Application US/11209206
; Publication No. US20060110794A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papill
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/11/209,206
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-11-209-206-6

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Query Match          19.7%; Score 102; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      27 QNDSSSEEDRIDGPAQA 46
Db      2 QNDSSSEEDRIDGPAQA 21

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RESULT 5
US-11-209-206-7
; Sequence 7, Application US/11209206
; Publication No. US20060110794A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papill
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/11/209,206
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-11-209-206-7

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Query Match          15.6%; Score 80.5; DB 7; Length 21;
Best Local Similarity 81.8%; Pred. No. 0.003;
Matches 16; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      18 ETTDLYXXQLNDSSEEDRID 39
Db      1 ETTDLYCYEQLNDS-SEEDID 21

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RESULT 6
US-11-293-697-2678
; Sequence 2678, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2678
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2678

Query Match
Best Local Similarity 12.1%; Score 62.5; DB 7; Length 148;
Matches 19; Conservative 5; Mismatches 21; Indels 17; Gaps 2;

QY 31 SSEEDDELIDGPAQAE-----DRAHNYITFCCKCDSTLRLCVQSTHVDIR 77
Db 50 SSSPESSSDGAGPEPTGSSGCTGSCWCSLSPVHSHMGMECP-----ILCCRSFHLHR 105
QY 78 TL 79
Db 106 GL 107

RESULT 7
US-10-505-928-341
; Sequence 341, Application US/10505928
; Publication No. US20060086532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 341
; LENGTH: 1287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-341

Query Match
Best Local Similarity 11.7%; Score 60.5; DB 6; Length 1287;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;

QY 23 YXXYQLNDSSEEDIDGPA-----GOAEPDRAHNYITFCCKCD 62
Db 1126 YGLQSSDSDSEDEPPDNADSKSEYLLNQLRSTPEQLGQKERSKNDHEIN-CSNCE 1184
QY 63 STLRLCVQSTHVDIRLTLEDL 82
Db 1185 SV-----GTNADPFLVANI 1198

RESULT 8
US-11-293-697-4473
; Sequence 4473, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
```

```
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4473
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4473

Query Match
Best Local Similarity 11.6%; Score 60; DB 7; Length 468;
Matches 29; Conservative 17; Mismatches 30; Indels 52; Gaps 7;

QY 16 QPETDLYXXYQLNDSSE-----EDEDIDGPAQAE-----QAEP----- 47
Db 35 EPQDLVWPRLNLSAEPQSLHPSRGVNNELPPQSGQGYGTRSRTPQSPHPTT 94
QY 48 -----DRAHNYITFCCKCDSTLRLCVQSTHVDIRLTLEDL-----MGTLGIVXP 92
Db 95 SSGNELPVVNSSAGSNCT--CNCSTLQAILQ-----ELKTRKLMQIQAVGTQNRQDP 148
QY 93 ---ICSQK 97
Db 149 ISLICSQR 156

RESULT 9
US-10-953-349-39521
; Sequence 39521, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39521
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39521

Query Match
Best Local Similarity 11.3%; Score 58.5; DB 6; Length 462;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTLHEMYLDLOPETDLYXXYQLNDSSE---ED-----EIDGPAQAEPPRAHNYI 54
Db 351 PAVHMASYDLGKAYDV-----LRQNSRFLLEBYRNPGFLQEGFGADSKP----- 398
QY 55 VTFCKCDSTLRLCVQSTHV--DIRLTLEDLMGTLGIYXPCSQ 96
Db 399 -----ISLCEVDODYGRIRKLOEYLEKYSIVPCSCQ 432

RESULT 10
US-10-953-349-39520
; Sequence 39520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
```

```

; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39520
; LENGTH: 616
; TYPE: PRY
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39520

```

Query Match	11.3%;	Score 58.5;	DB 6;	Length 616;
Best Local Similarity	23.1%;	Pred. No. 33;		
Matches	24;	Conservative	15;	Mismatches 30;
				Indels 35;
				Gaps 5;

```
QY      6 PTLHEMLDIQPETTDLYXXQINDSEEE---ED-----EIDPAGQAEBDDRAHANI 54
          |||         |||
DbB     505 PAVNMAVSDDLKGKADV----LRONSSRFLELDVYNRNPGLPFEPGPAADSKF----- 552
```

```
QY      55 VTFCCKDSTLRLCVQSTHV--DIRTLEDLLMGTLGIIVXPICSQ 96
          : ||: |::| | | | | |
DB      553 -----ISLCVEDDQDYMGRIKKLGLEYLEKYKSIKVPKGSQ 586
```

```

RESULT 11
US-10-953-39519
; Sequence 39519, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39519
;
; LENGTH: 646
;
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39519

```

Query March	11.3%	Score 58.51	DB 6	Length 646
Best Local Similarity	23.1%	Pred No. 35		
Matches	24	Conservative 15	Mismatches 30	Indels 35
			Gaps 5	

  

Qy	6	PTLHEMYMDLOPETTDLYXXYKQANDSSE	--ED-----	EIDPGCAQEPEDRAHYNI	54
Db	535	PAVMAASVADLGKAYDV-----	LRONSSRFLEEDYRNPNGLPQFGPADSKP	-----	582
Qy	55	VTFCCKDSTLRLCVQSTHV--	DIITLEDLIMGLGIYPICSQ	96	
Db	583	-----ISLCEVDODYMGRIKLOEYLEKXVSIKPGSQ	616		

```

RESULT 12
US-10-953-349-27426
; Sequence 27426, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: ParentIn version 3.3
; SEQ ID NO 27426
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-27426

```

	Query Match	Similarity	Score	DB	Length
Db	16; Conservative	27.6%;	57.5;	6;	233;
	Matches	11; Mismatches	24; Indels	7; Gaps	2;
Qy	8 LHEYML-DLQETTDLLXXXXQNDSSSEDEIDGSPAGAEEDRAHYNIVTFCKCDST	64			
	85 IQEYVLGEPYDDADDAVHDNHTSSAEEDHYKD-----TSKRHHVYNTNGTVCDDL	136			

RESULT 13  
US-10-953-349-27425

; Publication No. US20060107345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALEXANDROV, Nikolai et al.  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

```

; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

```

```

; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-953-349-27425

```

Query Match 11.1%; Score 57.5; DB 6; Length 296;  
Best Local Similarity 27.6%; Pred. No. 19;  
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;

QY 8 LHEWML-DLQPEFTDLVXXYLNDSSSEEDIEDGAGAEPPRAHYNIIVTFCKCDST 64  
: |: : |: : ::|: : | : ||  
Db 148 IQEYVLGEYPDPAITDAIHDNHTSSADEBIVKD-----TSKRYHHNYTNGVICDLT 199

```

RESULT 14
US-10-953-349-27424
; Sequence 27424, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27424
;
; LENGTH: 353
;
; TYPE: PRT
;
; ORGANISM: Triticum aestivum
US-10-953-349-27424

```

	Query Match	Similarity	11.1%	Score	57.5	DB	6	Length	353
	Best Local	Similarity	27.6%	Pred.	No. 23				
	Matches	Conservative	11	Mismatches	24	Indels	7	Gaps	2
Oy	8	LHEYML-DLOPETTDLYXXYOQNDSSSEDEIDGPAQAQBDRHAYNIIVTFCKCDST	64						
	:	: ::  :							
Dd	205	IQRVLVSYPDPADDAVHDNHTSSAEDHYKD-----TSKRHHAVYVTNGTVCIDL	256						
	:	::  :: :							

RESULT 15  
 US-10-953-349-39537  
 ; Sequence 39537, Application US/10953349  
 ; Publication No. US20060107345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALEXANDROV, Nickolai et al.  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 ; TITLE OF INVENTION: ENCODED THERAPY



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## OM protein - protein search, using sw model

Run on: June 6, 2006, 12:05:01 ; Search time 19.8916 Seconds

(without alignments)  
499.124 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517  
Sequence: 1 MHGDTPTLHEVMDLQPEPTT.....LEDLIMGTLGIYVPICSQKP 98Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	512	99.0	98	1	W7MLHS E7 protein - human
2	381.5	73.8	98	1	W7MLJ3 E7 protein - human
3	372	72.0	98	1	W7MLJ1 E7 protein - human
4	295	57.1	97	1	W7MLJ3 E7 protein - human
5	294	56.9	99	2	S36574 E7 protein - human
6	289.5	56.0	98	1	W7ML58 E7 protein - human
7	245	47.4	98	1	W7ML11 E7 protein - human
8	243	47.0	98	1	W7ML6 E7 protein - human
9	222.5	43.0	97	2	S36516 E7 protein - human
10	218.5	42.3	113	1	W7MLR1 E7 protein - human
11	213	41.2	106	2	S36562 E7 protein - human
12	209.5	40.5	105	2	S36504 E7 protein - human
13	208.5	40.3	105	2	S36528 E7 protein - human
14	200.5	38.8	101	1	W7MLJ3 E7 protein - human
15	200.5	38.8	105	1	W7ML18 E7 protein - human
16	194	37.5	98	1	W7MLC1 E7 protein - human
17	183.5	35.5	93	1	W7ML42 E7 protein - human
18	183.5	35.5	105	2	B44890 E7 protein - human
19	178.5	34.5	92	1	S15622 E7 protein - human
20	178.5	34.5	105	2	S36580 E7 protein - human
21	178.5	34.5	111	2	S36585 E7 protein - human
22	178	34.4	101	1	W7ML51 E7 protein - human
23	175.5	33.9	92	1	S15615 E7 protein - human
24	173.5	33.6	86	2	S36533 E7 protein - human
25	170	32.9	95	2	S36480 E7 protein - human
26	170	32.9	109	1	W7ML39 E7 protein - human
27	169	32.7	104	2	S36510 E7 protein - human
28	166.5	32.2	92	2	S36498 E7 protein - human
29	157.5	30.5	110	1	W7MLPR E7 protein - human

30	150.5	29.1	111	2	S36556 E7 protein - human
31	148	28.6	93	2	S36474 E7 protein - human
32	140.5	27.2	104	2	S36545 E7 protein - human
33	138	26.7	93	1	W7ML E7 protein - human
34	122	23.6	93	2	S36591 E7 protein - human
35	120.5	23.3	102	2	S36492 E7 protein - human
36	119	23.0	103	2	S36539 E7 protein - human
37	116.5	22.5	102	2	S36486 E7 protein - human
38	113	21.9	103	1	W7ML47 E7 protein - human
39	112	21.7	103	1	W7ML5 E7 protein - human
40	109	21.1	103	1	W7MLB5 E7 protein - human
41	105	20.3	103	1	W7ML8 E7 protein - human
42	87	16.8	94	1	W7MLRB E7 protein - human
43	83.5	16.2	98	2	B61399 E7 protein - human
44	80	15.5	55	2	S19907 E7-C protein - human
45	79.5	15.4	98	2	A61399 early protein E7 -

## ALIGNMENTS

## RESULT 1

W7MLHS  
E7 protein - human papillomavirus type 16  
C:Species: human papillomavirus type 16  
C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
C:Accession: A03688; S12367; T10428  
R:Seedorf, K.; Kramer, G.; Durest, M.; Suhai, S.; Rowekamp, W. G.  
Virology 145, 181-185, 1985  
A:Title: Human papillomavirus type 16 DNA sequence.  
A:Reference number: A22355; MUID:85246220; PMID:2990099  
A:Accession: A03688  
A:Molecule type: DNA  
A:Residues: 1-98 <SEES>  
A:Cross-references: UNIPROT:P03129; UNIPARC:UPI00000034E; GB:K02718; NID:G333031; PIDN:EMBL:K02718; NID:G333031; PIDN:AAAA6940.1; PI  
EMBO J. 9, 153-160, 1990  
A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large  
A:Reference number: S12367; MUID:90107938; PMID:2153075  
A:Accession: S12367  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-98 <BAR>  
A:Cross-references: UNIPARC:UPI00000034E  
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.  
J. Virol. 65, 2093-2097, 1991  
A:Title: A negative element in the human papillomavirus type 16 genome acts at the level  
A:Reference number: Z17014; MUID:91162763; PMID:1848319  
A:Accession: T10428  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-98 <KEN>  
A:Cross-references: UNIPARC:UPI00000034E; EMBL:K02718; NID:G333031; PIDN:AAAA6940.1; PI  
C:Gene: E7  
C:Superfamily: Papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger  
F:58-94/Region: zinc finger CCCC motif

Query Match 99.0%; Score 512; DB 1; Length 98;  
Best Local Similarity 96.9%; Pred. No. 6.2e-50;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEVMDLQPEPTTLDYXXQLNDSSEEDIDGPAGQAEPPRAHYNIYTFCK 60  
DB 1 MHGDTPTLHEVMDLQPEPTTLDYCYEQUNDSSEEDIDGPAGQAEPPRAHYNIYTFCK 60  
QY 61 CDSTRLCVOGSTRVDIRTLIEDLIMGTLGIYVPICSQKP 98  
DB 61 CDSTRLCVOGSTRVDIRTLIEDLIMGTLGIYVPICSQKP 98  
QY 61 CDSTRLCVOGSTRVDIRTLIEDLIMGTLGIYVPICSQKP 98  
DB 61 CDSTRLCVOGSTRVDIRTLIEDLIMGTLGIYVPICSQKP 98  
RESULT 2

M7ML35  
E7 protein - human papillomavirus type 35  
C:Species: human papillomavirus type 35  
A:Note: host Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: F40824; S36522  
R:Marich, J.E.; Ponteleir, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virology 186, 770-776, 1992  
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papilloma-  
A:Reference number: A40824; MUID:92124753; PMID:1310198  
A:Accession: F40824  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-99 <MAR>  
A:Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:G333050; PIDN:  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36522  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-99 <DEL>  
A:Cross-references: UNIPARC:UPI000000035E; EMBL:X74477; NID:G36997; PIDN:CAA5262.1; PR  
A:Experimental source: strain 35H  
C:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger  
P:59-95/Region: zinc finger CCCC motif

Query Match	Similarity	73.8%	Score 381.5	DB 1	Length 99
Beet	Local	73.5%	Pred. 2.2e-35		
Matches	72	Conservative 11	Mismatches 14	Indels 1	Gaps 1
Qy	1	MHGDTPTLHEMYLMDLPETPTDLYXXQLNDSS-EBEDEIDSPAGQAEPRAHNIIVTFC	59		
Dy	1	MHGDTTLPQVPLDLPEDATDLYCEQLCDSSEEDDTDDSPAGQAKPTTSNNIVTSC	60		
Qy	60	KCDSTLRLCVOSTHVDIRTLEDLLMGTILGIVXPICSR	97		
Dy	61	KCEATRLRCVOSTHDIRKLEDLLMGTGIVCPGCSR	98		

RESULT 3  
W7MLJ1  
E7 protein - human papillomavirus type 31  
C:Species: human papillomavirus type 31  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C:Accession: B32444  
R:Goldborough, M.D.; Dislivestre, D.; Temple, G.F.; Lorincz, A.T.  
Virology 171, 306-311, 1989  
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated  
A:Reference number: A94398; MUID:89299478; PMID:2545036  
A:Accession: B32444  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-58 <GOL>  
A:Cross-references: UNIPROT:P17387, UNIPARC:UPI000013840A; GB:J04355; NID:G9333046; PTDN:  
C:Comment: This protein may be involved in the oncogenic potential of this virus.  
C:Superfamily: Papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger  
/58-94/Region: zinc finger CCCC motif

[illegible]

Db 61 CKSTRLCVQSTQVDIRILQELMGSGFIVCPNCSTR 97

## RESULT 4

E7 protein - human papillomavirus type 33  
 C:Species: human papillomavirus type 33  
 C:Date: 30-Jun-1987 #sequence revision 30-Jun-1987 #text\_change 09-Jul-2004  
 C:Accession: A03689; S23831; S23827  
 R:Cole, S.T.; Strebeck, R.E.  
 J. Virol. 58, 991-995, 1986  
 A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which  
 A:Reference number: A93020; MUID:86200464; PMID:300902  
 A:Accession: A03689  
 A:Molecule type: A  
 A:Residues: 1-97 <SNI>  
 A:Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; GB:M12733; NID:G33049; PIDN:  
 R.Snijders, P.J.F.; van den Brule, A.J.C.; Schijtmakers, H.F.J.; Raaphorst, P.M.C.; Me  
 submitted to the EMBL Data Library, January 1992  
 A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via tw  
 A:Reference number: S19906  
 A:Accession: S23831  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-97 <SNI>  
 A:Cross-references: UNIPARC:UPI000013840C; EMBL:X64085; NID:G60278; PIDN:CAA45434.1; PID  
 C:Superfamily: papillomavirus E7 protein  
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger  
 P:58-94/Region: zinc finger CCCC motif

	Query Match	57.1%;	Score 295;	DB 1;	Length 97;
	Best Local Similarity	57.7%;	Pred. No. 9.4e-26;		
	Matches	56;	Conservative 16;	Mismatches 25;	Indels 0; Gaps 0;
QY	1	MAGDPPTLHEVMDLPETTTDLYXXQLNDSSEEDBEIDGPAQAGPBRRAHYNIVTFCK	60		
Db	1	MRGHKPTLKEVYLDLYPEPTDLYCYEQLSDSDSEDEGLDRPDQAGPATDYYIVTCHT	60		
QY	61	CDSTLRLCVQSTHVDIRTLIEDLLMGTGLVXPICGK	97		
Db	61	CNTIVRLCNSTASDLRTIQQLIMGTGVNIVCPCCAQ	97		

```

RESULT 5
S36574
E7 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C>Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S36574
R:Delius, H.; Hofmann, B.
A:Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36574
A:Molecule type: DNA
A:Residues: 1-99 <DBL>
A:Cross-references: UNIPROT:P36831; UNIPARC:UPI000013841C; EMBL:X74481; NID:g397038; PIDD:
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          56.9%; Score 294; DB 2; Length 99;
Best Local Similarity 57.1%; Pred. No. 1,2e-25;
Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

```

QY	1	MAGDTPTLHEWLDLOPETTDLXXYYQLNDSSEEDB--IDPAGQAEPBRAHNIATFC	58
Dd	1	MKGDAITIKDYLDLOPETTDLCYEQLDSSSBETDGDGRDPGGAQOATSNIYIATC	60
QY	59	CKCDSTLRICVOSTHVDIRTLEDLMGTIGIAYPICSQ	96
Dd	61	HSCDSTLRICINSTATDTRLQOMLLGTLOAVPCGAR	98



## RESULT 6

W7ML58

E7 protein - human papillomavirus type 58

C:Species: human papillomavirus type 58

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004

C:Accession: F36779

R:Kiril, Y.; Iwamoto, S.; Matsukura, T.

Virology 185, 424-427, 1991

A:Title: Human papillomavirus type 58 DNA sequence.

A:Reference number: A36779; MUID:92024102; PMID:1656594

A:Accession: F36779

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-58 &lt;KIR&gt;

A:Cross-references: UNIPROT:P26557; UNIPARC:UPI000000344B; GB:D90400; NID:G222386; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:59-95/Region: zinc finger CCCC motif

Query Match 56.0%; Score 289.5; DB 1; Length 98;

Best Local Similarity 57.1%; Pred. No. 3.9e-25;

Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 1 MHGDPPTHEWMLDQPERTDLYXXQLNDSSEED-DEIDGPAQAEPRAHYNIYVTC 59

Db 1 MGNPPTREYILDHPETDPCYBQLCDSDEDEIGDGPDAQPATANYIVTCCY 60

Qy 60 KCDSTLRCLVQSTHVDIRTLDELMLGTLGIYXPCISOK 97

Db 61 TCGTIVRLCINSTTDDVRLQQLMGTCITVPSCAQ 98

## RESULT 7

W7ML1

E7 protein - human papillomavirus type 11

C:Species: human papillomavirus type 11

C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004

C:Accession: A03690

R:Datman, K.; Schwartz, E.; Gissmann, L.; zur Hausen, H.

Virology 151, 124-130, 1986

A:Title: The nucleotide sequence and genome organization of human papilloma virus type 1

A:Reference number: A03690; MUID:86181601; PMID:3008427

A:Accession: A03690

A:Molecule type: DNA

A:Residues: 1-98 &lt;DAR&gt;

A:Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:G333026; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 47.4%; Score 245; DB 1; Length 98;

Best Local Similarity 53.0%; Pred. No. 3.5e-20;

Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

Qy 1 MHGDPPTHEWMLDQ-BETDLYXXQLNDSSEED-DEIDGPAQAEPRAHYNIYVTC 58

Db 1 MHGRLVTKDVLIDQPPDPVGLHCYEQLESSEBEVKVD--KODAPLTQHYOILTC 58

Qy 59 CKDSTLRCLVQSTHVDIRTLDELMLGTLGIYXPCISOK 98

Db 59 CGCDSNRLVVECTDGRQDLGLGLTIVCPICAPK 98

## RESULT 8

W7ML6

E7 protein - human papillomavirus type 6b

C:Species: human papillomavirus type 6b

C:Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004

C:Accession: D20558

R:Schwarz, E.; Durec, M.; Demankowski, C.; Laternmann, O.; Zech, R.; Wolfspurger, E.; Su

EMBO J. 2, 2341-2348, 1983

A:Title: DNA sequence and genome organization of genital human papillomavirus type 6b.

A:Reference number: A09075; MUID:84131949; PMID:6321162

A:Accession: D20558

A:Molecule type: DNA

A:Residues: 1-98 &lt;SCH&gt;

A:Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:G60955; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 47.0%; Score 243; DB 1; Length 98;

Best Local Similarity 52.5%; Pred. No. 5.9e-20;

Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

Qy 1 MHGDPPTHEWMLDQ-BETDLYXXQLNDSSEED-DEIDGPAQAEPRAHYNIYVTC 58

Db 1 MHGRLVTKDVLIDQPPDPVGLHCYEQLESSEBEVKVD--DSQPLKQHFQIVTCC 58

Qy 59 CKDSTLRCLVQSTHVDIRTLDELMLGTLGIYXPCISOK 97

Db 59 CGCDSNRLVVECTDGRQDLGLGLTIVCPICAPK 97

## RESULT 9

S36516

E7 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36516

R:Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36516

A:Molecule type: DNA

A:Residues: 1-97 &lt;DEL&gt;

A:Cross-references: UNIPROT:P36828; UNIPARC:UPI000013840D; EMBL:X74476; NID:G396989; PII

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 43.0%; Score 222.5; DB 2; Length 97;

Best Local Similarity 49.0%; Pred. No. 1.1e-17;

Matches 48; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

Qy 1 MHGDPPTHEWMLDQERT-IDLYXXQLNDSSEED-DEIDGPAQAEPRAHYNIYVTC 59

Db 1 MHGKPSQDVLIDKPTERTDLCYEST-DSSEDETDSTL-ERQAEQAWYRVTPCS 58

Qy 60 KCDSTLRCLVQSTHVDIRTLDELMLGTLGIYXPCISOK 97

Db 59 KQSTVCLTSTHADVLDLVDLMLGALKIVCPNCSRR 96

## RESULT 10

W7ML1

E7 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C:Accession: B38503

R:Ostrow, R.S.; Labreth, K.V.; Faras, A.J.

Virology 181, 424-429, 1991

A:Title: Characterization of the complete Rhyv 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: B38503

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-113 &lt;OST&gt;

A:Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 42.3%; Score 218.5; DB 1; Length 113;

Best Local Similarity 43.8%; Pred. No. 3.7e-17;

Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

```

Oy      1 MHGDTPTLHEWMLD-----QETTDLYXXYNQDSSSEDETDGPAQAEPDRAH----- 51
Db      1 MIGKPTLEDTEDVLQPPQPQPDVLMCEYDLSSESEDEVDHHNNNQOHHQHAREEV 60

Oy      52 -----YIVTFECCKDSTLRLCVQSTHVDLRTEEDLMGTGIVXPICSOK 97
Db      61 PEDGDCYRIVSDCYSCGKPLRLVWVSSHEDRLVEDLMGLTDIVCPSCASR 112

RESULT 11
S36562
E7 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36562
R:DeJans, H.; Hofmann, B.
A:Description: to the EMBL Data Library, August 1993
A:Reference number: S36469
A:Accession: S36562
A:Molecule type: DNA
A:Residues: 1-106 <DEL>
A:Cross-references: UNIPROT:P21736; UNIPARC:UPI0000138416; EMBL:X74479; NID:9397022; PIR:
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

```

```

Query Match          41.2%; Score 213; DB 2; Length 106;
Best Local Similarity 43.8%; Pred. No. 1.4e-16;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

OY 1 MHGDPPTLHEWMLDLOPET-----TDLYXXYXQLNDSSEEDSIDG-----PAGQAEPPDRAH- 50
Db 1 MHGRETIQELVHLHEPQNEIDPVDLYCEIDLSSEEDNEADQVSHQLPARRAEQFR- 59
OY 51 HNIIVTFCKCDSTLRKCVOSTHVDIRTLIEDLLMGTIGIYXPICS 95
Db 60 -HKLICVCKCDGRIELTVSESSAEIDLRTYLOQLFSTLSFVCPWCA 103

RESULT 12
S36504
E7 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36504
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36504
A:Molecule type: DNA
A:Residues: 1-105 <DEL>
A:Cross-references: UNIPROT:P36826; UNIPARC:UPI0000138409; EMBL:X74474; NID:G396973; PII
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          40.5%; Score 209.5; DB 2; Length 105;
Best Local Similarity 45.2%; Pred. No. 3.5e-16;
Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

OY 1 MHGDPPTLHEWMLDLOPET-TDLYXXYXQLNDSSE-EEIDG---PAGQAEPPDRAH--YN 53
Db 1 MHGAVTTIPETIYLDLVPGTEIDLHCEYEQANSSEEDDEEVNVLQKQPGQARQEGHCYCL 60
OY 54 IVTFCKCDSTLRKCVOSTHVDIRTLIEDLLMGTIGIYXPICSQK 97
Db 61 INFOCCRCASAVQLAVOSPTELRALQOMLMGALVELVCPICATR 104

RESULT 13
S36528
S7 protein - human papillomavirus type 53

```

C|Species: human papillomavirus type 53  
C|Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C|Accession: S36528  
R|DeJius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A|Description: Primer-directed sequencing of human papillomavirus types.  
A|Reference number: S36469  
A|Accession: S36528  
A|Molecule type: DNA  
A|Residues: 1-105 <DEL>  
A|Cross-references: UNIPROT:P36832; UNIPARC:UPI000013841D; EMBL:X74482; NID:g397046; PID:  
C|Superfamily: papillomavirus E7 protein  
C|Keywords: DNA binding; early protein; transcription regulation

Query Match	40.3%	Score 208.5	DB 2	Length 105
Best Local Similarity	43.3%	Pred. No. 4.5e-16		
Matches	45	Conservative 23	Mismatches 29	Indels 7
			Gaps 4	
QY	1	MAGDPTLTENYLDLPET-TDLYXXQLNDS-SEEDIED---	GPAGQAEPPDAH--YN	53
Db	1	MGNVPPTLQYXITIELPQTEIDLQCHEQLNDSSEDEDEDEVDYHQAEPQARARQHECYL		60
QY	54	IVTPCKDSTRLACVOSTHVDIRLTEDLMGLGIVXPICSQ		97
Db	61	IFTQCRCESTLVQAVQSSSTKEIRLQOMLMGVELVCPICATR		104

RESULT 14  
W7ML13  
E7 protein - human papillomavirus type 13.  
C:Species: human papillomavirus type 13  
A>Note: host Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 09-Jul-2004  
C:Accession: B42955  
R:van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G  
Virology 190, 587-596, 1992  
A:Title: Human papillomavirus type 13 and pYGM chimpanzee papillomavirus type 1: Comparison  
A:Reference number: A42955; MUID:92391075; PMID:132567  
A:Accession: B42955  
A:Molecule type: DNA  
A:Residues: 1-101 <V>AN>  
A:Cross-references: UNIPROT:Q02271, UNIPARC:UP100001383F9, EMBL:X62843, NID:960295, PIDN  
A:Superfamily: papillomavirus E7 protein  
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger  
F:61-97/Region: zinc finger CCCC motif

```

Query Match          38.8%; Score 200.5; DB 1; Length 101;
Best Local Similarity 44.7%; Pred. No.3.3e-15;
Matches             46; Conservative 13; Mismatches 35; Indels 9; Gaps 2;

Qy      1 MHGDPPTLHEWMLDOPETTDLYXXYXQLNDSSEBDEIOGPAGAEPRRAH-----YNI 54
        ||| ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       1 MHGKIPFLKDYLIELTPDPVGLHCNEQLDSS---EEBEVBQAQATQATGHSTLLCYOI 57
        ||| ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy      55 VTFCCCKDSTLRLCVOSTHVDIRTELDLMGTIGIYXPICISOK 97
        ||| ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       58 LTSCSKCCSNVRLVVECTSPDIHDHLDLGLTINIVCPICAPK 100
        ||| ||| : : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 15
w7m1l8
E7 protein - human papillomavirus type 18
C.Species: human papillomavirus type 18
C.Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #ext_change 09-Jul-2004
C.Accession: B26165; H26251
R.Sesdorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A>Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A.Reference number: A91068; MUID:87218459; PMID:3034571
A.Accession: B26165
A.Molecule type: DNA
A.Residues: 1-105 <SEE>
A.Cross-references: UNIPROT:P06788; UNIPARC:UPI0000000DB5; GB:X04773; NID:g60876; PIDN:CI

```

R: Cole, S.T.; Danos, O.  
J. Mol. Biol. 193, 599-608, 1987  
A: Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1  
A: Reference number: A92937; MUID: 87283882; PMID: 3039146  
A: Accession: H26251  
A: Molecule type: DNA  
A: Residues: 1-105 <COL>  
A: Cross-references: UNIPARC:UPI00000000B5; GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G  
C: Superfamily: Papillomavirus E7 protein  
C: Keywords: DNA binding; early protein; transcription regulation  
Query Match 38.8%; Score 200.5; DB 1; Length 105;  
Best Local Similarity 39.6%; Pred. No. 3.5e-15;  
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;  
QY 1 MHGDTPTLHEYMLDLPET--TDLYXXYQLNDSSEDEIDG-----PAGQAEPPRAH 51  
DB 1 MHGPRATLDIVLHLEPQWEIPVDLLCHEQLSDSEBENDEIDGVNHHLPARRAEPR-- 58  
QY 52 YNIVTFCKCKDSTLRCLCVOSTHVDIRITLEDLMGTLGIYXPTCSOK 97  
DB 59 HTMLCMCKCKCEARIELVVESSADDLRAFOQLFLNTLSFVCPWCASQ 104

Search completed: June 6, 2006, 12:11:54  
Job time : 18.8916 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:34 ; Search time 151.133 Seconds  
(without alignments)  
599.815 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517

Sequence: 1 MHGDPPTLHEVWLDPERT.....LEDLMGTLLGIVXPICGQKP 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_crembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	1	VE7 HPV16
2	512	99.0	98	2	054788 HPV16
3	512	99.0	98	2	Q77864 HPV16
4	512	99.0	98	2	Q77866 HPV16
5	512	99.0	98	2	Q77868 HPV16
6	512	99.0	98	2	Q77869 HPV16
7	512	99.0	98	2	Q77881 HPV16
8	512	99.0	98	2	Q77882 HPV16
9	512	99.0	98	2	Q77887 HPV16
10	512	99.0	98	2	Q77889 HPV16
11	512	99.0	98	2	Q77810 HPV16
12	512	99.0	98	2	Q77811 HPV16
13	512	99.0	98	2	Q77813 HPV16
14	512	99.0	98	2	Q77815 HPV16
15	512	99.0	98	2	Q77817 HPV16
16	512	99.0	98	2	Q77819 HPV16
17	508	98.3	98	2	Q12337 HPV16
18	507	98.1	98	2	Q11650 HPV16
19	507	98.1	98	2	Q77883 HPV16
20	507	98.1	98	2	Q77885 HPV16
21	507	98.1	98	2	Q68RD2 HPV16
22	507	98.1	98	2	Q68RD3 HPV16
23	507	98.1	98	2	Q2MJT3 HPV16
24	504	97.5	98	2	Q12338 HPV16
25	500	96.7	98	2	Q8V1J0 HPV16
26	499	96.5	98	2	Q68RD4 HPV16
27	486	94.0	94	2	Q8B5P6 HPV16
28	478	92.5	93	2	Q9QDH2 HPV16
29	477	92.3	93	2	Q9QDH4 HPV16
30	477	92.3	93	2	Q9QDH6 HPV16
31	477	92.3	93	2	Q9QDH8 HPV16

32	406	78.5	77	2	Q8B5P5 HPV16	Q8B5P5 human papill
33	381.5	73.8	99	1	VE7 HPV35	P27230 human papill
34	381.5	73.8	99	2	Q76WP2 HPV16	P17387 human papill
35	372	72.0	98	1	VE7 HPV31	Q6C377 human papill
36	367	71.0	98	2	Q6C377 HPV31	Q8B563 HPV16
37	343	66.3	65	2	Q8B563 HPV16	Q90724 human papill
38	316	61.1	99	2	Q90724 HPV16	P06429 human papill
39	295	57.1	97	1	VE7 HPV33	P36831 human papill
40	294	56.9	99	1	VE7 HPV52	P26557 human papill
41	289.5	56.0	98	2	Q547M4 HPV58	Q547M4 human papill
42	289.5	56.0	98	2	Q9QCZ1 HPV58	Q9QCZ1 human papill
43	288.5	55.8	98	2	Q8QSF0 HPV58	Q8QSF0 human papill
44	286.5	55.4	98	2	Q8QHN7 HPV58	Q8QHN7 human papill
45	285.5	55.2	98	2	Q8QHN7 HPV58	Q8QHN7 human papill

## ALIGNMENTS

RESULT 1  
VE7 HPV16 STANDARD; PRT; 98 AA.  
AC P03129;  
DT 21-JUL-1966, integrated into UniprotKB/Swiss-Prot.  
DT 21-JUL-1966, sequence version 1.  
DT 07-FEB-2006, entry version 43.  
DE Protein E7.  
GN Name=E7;  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBT:taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=85246220; PubMed=2990099;  
RA Seedorf K., Krammer G., Durst M., Subai S., Roweckamp W.G.;  
RT "Human papillomavirus type 16 DNA sequence.";  
RL Virology 145:181-185(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=90218027; PubMed=2157796;  
RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;  
RT "Expression of the human papillomavirus type 16 genome in SK-V cells, a line derived from a vulvar intraepithelial neoplasia.";  
RL J. Gen. Virol. 71:809-817(1990).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;  
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX Torresello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,  
RA Beth-Giraldo E., Giraldo G.;  
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=Isolate African 1, and isolate European German 131;  
RA Terai M., Fu L., Ma Z., Burk R.D.;  
RT "Cloning and sequencing of non-European human papillomavirus (HPV) variant complete genomes from cervicovaginal cells by an overlapping PCR method.";  
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP FUNCTION.  
RX MEDLINE=88223347; PubMed=2836062;  
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;  
RT "The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A.";  
CC Cell 53:539-547(1988).  
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.  
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC -----  
DR EMBL: K02718; AAA46940.1; -; Genomic DNA.  
DR EMBL: D00735; BAA00633.1; -; Genomic DNA.  
DR EMBL: U76411; AAB18962.1; -; Genomic DNA.  
DR EMBL: U76412; AAB18963.1; -; Genomic DNA.  
DR EMBL: U76413; AAB18964.1; -; Genomic DNA.  
DR EMBL: AF003020; AAB70737.1; -; Genomic DNA.  
DR EMBL: AF003023; AAB70740.1; -; Genomic DNA.  
DR EMBL: AF003024; AAB70741.1; -; Genomic DNA.  
DR EMBL: AF003025; AAB70742.1; -; Genomic DNA.  
DR EMBL: AF003026; AAB70743.1; -; Genomic DNA.  
DR EMBL: AF536179; AAQ10713.1; -; Genomic DNA.  
DR EMBL: AF536180; AAQ10721.1; -; Genomic DNA.  
DR PIR: A03688; W7MLHS.  
DR InterPro: IPR000149; Papv\_E7.  
DR Pfam: PF00527; E7; 1.  
KW DNA-binding; Early protein; Oncogene; Transcription;  
KW Transcription regulation.  
FT CHAIN 1 Protein E7.  
FT MOTIF 58 61 /Frid=PRO\_0000133414.  
FT MOTIF 91 94 C-XX-C motif-1.  
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
C-XX-C motif-2.  
Query Match 99.0%; Score 512; DB 1; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLQETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 1 MHGDTPTLHEYMLDLQETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98  
DB 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98

RESULT 2  
ID 054788 HPV16 PRELIMINARY; PRT; 98 AA.  
AC 054788;  
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 24-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
GN Name=E7;  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Zhang, J, Gao, Y, Yan X.;  
RT "Cloning and sequence analysis of Human papillomavirus type 16 E7 gene  
RT in China.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC -----  
DR EMBL: AF512012; AAM74160.1; -; Genomic DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
FT NON TER 98  
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLQETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 1 MHGDTPTLHEYMLDLQETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98  
DB 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98

RESULT 3  
ID 07864 HPV16 PRELIMINARY; PRT; 98 AA.  
AC 07864;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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CC -----  
DR EMBL: AJ388069; CAB45131.1; -; Genomic DNA.  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv\_E7.  
DR Pfam: PF00527; E7; 1.  
FT NON TER 98  
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLQETTTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60  
DB 1 MHGDTPTLHEYMLDLQETTTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60

QY 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98  
DB 61 CDSTLRLCVOSTHVDIRLTEDLLMGTGIGVXPICSQKP 98

RESULT 4  
ID 07866 HPV16 PRELIMINARY; PRT; 98 AA.  
AC 07866;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI\_Taxid=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

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RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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CC -----  
CC EMBL: AJ388068; CAB45129.1; -; Genomic_DNA.  
CC  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON_TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
SQ  
  
Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MHGDTPTLHEHYMLDLPETTDLYXXYQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDTPTLHEHYMLDLPETTDLYCYEQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
1 CDSTRLCVOSTHVDIRTELDLGMGTGIVXPICSQKP 98  
61 CDSTRLCVOSTHVDIRTELDLGMGTGIVCPICSQKP 98  
Db  
  
RESULT 5  
Q778G8 HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q778G8;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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CC -----  
CC EMBL: AJ388067; CAB45127.1; -; Genomic_DNA.  
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DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON_TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
SQ  
  
Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MHGDTPTLHEHYMLDLPETTDLYXXYQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDTPTLHEHYMLDLPETTDLYCYEQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
1 CDSTRLCVOSTHVDIRTELDLGMGTGIVXPICSQKP 98  
61 CDSTRLCVOSTHVDIRTELDLGMGTGIVCPICSQKP 98  
Db  
  
RESULT 6  
Q778G9 HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q778G9;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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CC -----  
CC EMBL: AJ388066; CAB45125.1; -; Genomic_DNA.  
CC  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON_TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
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Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MHGDTPTLHEHYMLDLPETTDLYXXYQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDTPTLHEHYMLDLPETTDLYCYEQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
1 CDSTRLCVOSTHVDIRTELDLGMGTGIVXPICSQKP 98  
61 CDSTRLCVOSTHVDIRTELDLGMGTGIVCPICSQKP 98  
Db  
  
RESULT 7  
Q778H1 HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q778H1;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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Db 61 CDSTRLCVOSTHVDIRTELDLGMGTGIVCPICSQKP 98  
  
RESULT 6  
Q778G9 HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q778G9;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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CC -----  
CC EMBL: AJ388066; CAB45125.1; -; Genomic_DNA.  
CC  
DR GO: GO:0005622; C:intracellular; IEA.  
DR GO: GO:0003700; F:transcription factor activity; IEA.  
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR000148; Papv1_E7.  
DR Pfam: PF00527; E7; 1.  
DR NON_TER 98  
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;  
SQ  
  
Query Match 99.0%; Score 512; DB 2; Length 98;  
Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 1 MHGDTPTLHEHYMLDLPETTDLYXXYQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
Db 1 MHGDTPTLHEHYMLDLPETTDLYCYEQQLNDSSEEDSIDGPAGQAEPPRAHNYITVFCCK 60  
1 CDSTRLCVOSTHVDIRTELDLGMGTGIVXPICSQKP 98  
61 CDSTRLCVOSTHVDIRTELDLGMGTGIVCPICSQKP 98  
Db  
  
RESULT 7  
Q778H1 HPV16 PRELIMINARY; PRT; 98 AA.  
AC Q778H1;  
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
DT 10-MAY-2005, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE E7 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Alphapapillomavirus.  
OX NCBI_TaxID=333760;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20112892; PubMed=10644829;  
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
RL J. Gen. Virol. 81:317-325(2000).  
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DR	EMBL; AJ388065; CAB45123.1; -; Genomic_DNA.
DR	GO; GO:00055622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR000148; Papvi_E7.
DR	Pfam; PF00527; E7; 1.
DR	NON TER
FT	NON TER
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 MHGDTPTLHETMLDLPETTTLDYXXYLQNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60       1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60
Dd	1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60       1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60
Oy	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98       61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98
Dd	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98       61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98
RESULT 9	
O778H7_HPV16	PRELIMINARY; PRT; 98 AA.
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AC O778H2;	
DT 10-MAY-2005,	integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005,	sequence version 1.
DT 07-FEB-2006,	entry version 3.
DE E7 protein (Fragment).	
OS Human papillomavirus type 16.	
OC Viruses; daDNA viruses, no RNA stage; Papillomaviridae;	
CC Alphapapillomavirus.	
OX NCBI_TaxID=333760;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RK MEDLINE=20112892; PubMed=10644829;	
RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).	
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DR EMBL; AJ388064; CAB45121.1; -; Genomic_DNA.	
DR GO; GO:00055622; C:intracellular; IEA.	
DR GO; GO:0003700; F:transcription factor activity; IEA.	
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR InterPro; IPR000148; Papvi_E7.	
DR Pfam; PF00527; E7; 1.	
DR NON TER	
FT NON TER	
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;	
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4.5e-52;
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Oy	1 MHGDTPTLHETMLDLPETTTLDYXXYLQNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60       1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60
Dd	1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60       1 MHGDTPTLHETMLDLPETTTLDYCYEQUNDSSSEEDSIDGPAGQAEPPRAHYNIIVTFCK 60
Oy	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98       61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98
Dd	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98       61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPCISQKP 98
RESULT 9	
O778H7_HPV16	PRELIMINARY; PRT; 98 AA.
ID O778H7_HPV16	PRELIMINARY; PRT; 98 AA.
AC O778H7;	
DT 10-MAY-2005,	integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005,	sequence version 1.
DT 07-FEB-2006,	entry version 3.
DE E7 protein (Fragment).	
OS Human papillomavirus type 16.	
OC Viruses; daDNA viruses, no RNA stage; Papillomaviridae;	
CC Alphapapillomavirus.	
OX NCBI_TaxID=333760;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RK MEDLINE=20112892; PubMed=10644829;	
RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).	
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DR GO; GO:0003700; F:transcription factor activity; IEA.	
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	
DR InterPro; IPR000148; Papvi_E7.	
DR Pfam; PF00527; E7; 1.	
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FT NON TER	
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;	

DT	10-MAY-2005, sequence version 1.
DT	07-FEB-2006, entry version 3.
DE	E7 protein (fragment).
OS	Human papillomavirus type 16.
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC	Alphapapillomavirus.
NCBI_TaxID=3333760;	
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20112892; PubMed=10644829;
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA	Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT	"Analysis of human papillomavirus type 16 E6 variants in relation to
RT	p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol.	81:317-325(2000).
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CC	-----
DR	EMBL; AJ388061; CAB45115.1; -; Genomic_DNA.
DR	GO; GO:0005622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	Pfam; PF00527; E7; 1.
FT	NON TER
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9BB CRC64;
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4,5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 MHGDPPTLHEWMLDLPETTTLYXXYXQLNDSESEDEIDGPAGGAEPRAHYNYTFCK 60
Db	1 MHGDPTLHEWMLDLPETTTLYCYEQUNDSSEDEIDGPAGGAEPRAHYNYTFCK 60
OY	61 CDSTLRLCVOSTHVDIRTELDLMGLTGIYPICSQKP 98
Db	61 CDSTLRLCVOSTHVDIRTELDLMGLTGIYPICSQKP 98
RESULT 10	
ID	Q778H9_HPV16 PRELIMINARY; PRT; 98 AA.
AC	Q778H9;
DT	10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT	10-MAY-2005, sequence version 1.
DE	07-FEB-2006, entry version 3.
DE	E7 protein (fragment).
OS	Human papillomavirus type 16.
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC	Alphapapillomavirus.
NCBI_TaxID=3333760;	
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20112892; PubMed=10644829;
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA	Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT	"Analysis of human papillomavirus type 16 E6 variants in relation to
RT	p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol.	81:317-325(2000)
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CC	-----
DR	EMBL; AJ388060; CAB45113.1; -; Genomic_DNA.
DR	GO; GO:0005622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	Pfam; PF00527; E7; 1.
FT	NON TER
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9BB CRC64;



Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
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Qy 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60  
 Db 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98  
 Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98

RESULT 11  
 ID 077810 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 077810;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 CC Alphapapillomavirus.  
 NX NCBI\_TaxID=3333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
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CC EMBL; AJ388059; CAB4511.1; -; Genomic\_DNA.  
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 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 FT NON TER 98  
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Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60  
 Db 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98  
 Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98

RESULT 12  
 ID 077811 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 077811;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 CC Alphapapillomavirus.  
 NX NCBI\_TaxID=3333760;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
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CC EMBL; AJ388058; CAB4510.1; -; Genomic\_DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 FT NON TER 98  
 FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60  
 Db 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98  
 Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPCISQKP 98

RESULT 13  
 ID 077813 HPV16 PRELIMINARY; PRT; 98 AA.  
 AC 077813;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 3.  
 DE E7 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 CC Alphapapillomavirus.  
 NX NCBI\_TaxID=3333760;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
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CC EMBL; AJ388057; CAB4510.1; -; Genomic\_DNA.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR000148; Papv1\_E7.  
 DR Pfam; PF00527; E7; 1.  
 FT NON TER 98  
 FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;  
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;  
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60  
 Db 1 MHGDPPTLHEVMDLPQETTTDLXXYXQUNDSSSEDEIDGPAGQAEPPRAHNYITVFCK 60

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QY 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVCPCISQKP 98

RESULT 14
077815 HPV16 PRELIMINARY; PRT; 98 AA.
ID 077815 HPV16
AC 077815;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC -----
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CC -----
DR EMBL; AJ388056; CAB45105.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003760; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR NON TR 98
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
SQ

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPETTDLYXXQUNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60

QY 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVCPCISQKP 98

RESULT 15
077811 HPV16 PRELIMINARY; PRT; 98 AA.
ID 077811 HPV16
AC 077811;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [2]
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RP NUCLEOTIDE SEQUENCE.
RA Duin M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AJ242681; CAB45382.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
DR NON TR 98
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
SQ

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEYMLDLPETTDLYXXQUNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60
Db 1 MHGDTPTLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGAEPPRAHYNIVTFCK 60

QY 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVXPCISQKP 98
Db 61 CDSTRLRCVOSTHVDIRTLBLLMGTLGIVCPCISQKP 98

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